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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents Ah:*
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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1525.031 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-182-859-6
US-09-264-097-8
US-09-672-459-6
US-10-186-042-6
US-10-186-042-7
US-09-537-168-17
US-09-537-168-9
US-08-459-610-6
US-08-459-610-6
US-08-683-38A-6
US-08-683-38A-6
US-08-683-6252A-6
US-08-683-6252A-6
US-09-386-252A-6
US-09-381-687-7
US-09-383-1687-7
US-09-383-158-3
US-09-170-670-3
US-09-183-412-3
US-09-184-3
US-09-184-3
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US-09-185-3
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Sequence 6, Appli
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Sequence 17, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 3, Appli
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US-09-182-859-6
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## ALIGNMENTS

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Sequence 6. Application US/09182859
Patent NO. 6143708
JERNERL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard: Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
JELE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-06-28
EARLIER FILING DATE: 1996-06-28
EARLIER FILING DATE: 1996-06-29
EARLIER REPLICATION NUMBER: 0775/96
EARLIER REPLICATION NUMBER: 1263/96
EARLIER APPLICATION NUMBER: 1263/96
EARLIER RETLING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
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; ORGANISM: Bacillus stearothermophilus
US-09-182-859-6
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                                          181 IGKAWDWEVDTENGNYDYLWYADLDNDHPEVVTELKNWGKWYVNTINIDGFRLDAVKHIK 240
                                                                                                                                                                               121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHEDGVDWDESRKLSRIYKFRG 180
                                                                                                                                  121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
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Gaps

60

241

FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300

240

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APPLICANT: No. 6287826man, Barrie Edmund
APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of Gli
TITLE OF INVENTION: From Starch
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 514
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Best Local Simi
Matches 514;
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Patent No. 6287826
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPFNGTMMQYFEWYLPDDGTLWTKVANBANNLSSLGITALWLPPAYKGTSRSDVGYGVY
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YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
                                                                                            SGGAFDMRTIMTUTIMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFIIITRQEG
                                                                                                                                                                                   FSFFFDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                                                                                                                                                                                                                            IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                                      IGXAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240
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                                                                                                                                                       FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300
                                                                                                                                                                                                                                                                                                                                   VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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Pred. No. 1.6e-245;
; Mismatches 0;
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Sequence 6, Application US/09672459

patent No. 643688

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
FRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0918/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
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PRIOR APPLICATION NUMBER: 1363/96
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APPLICANT: SVELUCEUR, CATALLA APPLICANT: Bisgard-Frantzen, Henrik APPLICANT: Bisgard-Frantzen, Henrik TITLE OF INVENTION: Alpha-Amylase Mutants FILE REFERENCE: 4796.204-US; CURRENT APPLICATION NUMBER: US/10/186,042; CURRENT FILING DATE: 2002-06-28; PRIOR APPLICATION NUMBER: US/09/672,459; PRIOR FILING DATE: 2000-09-28; PRIOR FILING DATE: 1998-10-29; PRIOR APPLICATION NUMBER: 0515/96; PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0775/96; PRIOR APPLICATION NUMBER: 0775/96; PRIOR APPLICATION NUMBER: 0775/96; PRIOR APPLICATION NUMBER: 075/96; PRIOR FILING DATE: 1996-07-11; PRIOR APPLICATION NUMBER: 075/96; PRIOR FILING DATE: 1996-07-10; PRIOR FILING DATE: 1996-07-11; PRIOR PRIOR PRIOR DATE: 1996-07-11; PRIOR PR
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Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
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(Sequence 17, Application US/09291023A)

Sequence 17, Application US/09291023A

Patent No. 6309871

(PARKATINE)

APPLICANT: Note of the content of the co
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                                    VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514
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RESULT 6 US-09-537-168-8

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Sequence 8, Application US/09537168
Fatent No. 6410295
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Christel T.
APPLICANT: Syendeen, Christel T.
APPLICANT: Syendeen, Allan
APPLICANT: Syendeen, Allan
TITLE OF INVENTION. Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT FALLING DATE: 2000-03-29
EARLIER APPLICATION NUMBER: US/09/537,168
CURRENT FILING DATE: 1999-03-30
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 515
Type: PRT
ORGANISM: Bacillus stearothermophilus
US-09-537-168-8
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Best Local Similarity 100.0%;
Matches 514; Conservative 0
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                 VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
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Pred. No. 1.6e-245;
); Mismatches 0;
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RESULT 7
US-09-540-715A-17
; Sequence 17, Application
; Patent No. 6623948

US/09540715A

Sequence 6, Application US/08720899
Patent No. 5753460
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Hen
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allam
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia

ANT: Bisgaard-Frantzen, Henrik ANT: Borchert, Torben Vedel ANT: Svendsen, Allan ANT: Thellersen, Marianne ANT: Van der Zee, Pia DF INVENTION: AMYLASE VARIANTS

RESULT 8 US-08-720-899-6

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APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vib&e
APPLICANT: Nielsen, Vib&e
APPLICANT: Hoeek, Lisbeth
ITILE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A:
ITILE OF INVENTION: Bocoding Same
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 515
TYPE: PRI
ORGANISM: Bacillus
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Matches 514; Conserv
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APPLICANT: Borchert, Tork
APPLICANT: Borchert, Tork
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100.0%; Pr
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Pred. No. 1.6e-245;
); Mismatches 0;
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Matches
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TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: US/08/
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STREET: New York
CITY: New York
TTATE: New York
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC COMPATIBLE PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECONCUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/343,804 FILING DATE: 22-NOV-1994 ATTORNEY/AGENT INFORMATION:
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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
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Pred. No. 1.7e-245;
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US-08-459-610-6
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; MOLECULE TYPE: protein US-08-459-610-6
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100
Matches 514; Conservative
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 4054.214-US
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
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COUNTRY: USA
ZIP: \0174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
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APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 405 Lexington Avenue, 64th CITY: New York
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241 FSFFPDWLSYVRSQTGKPLFTVGBYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300
                                                                                                                                                                                                                                                                                61 DLYDLGEFNQXGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 120
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                                                                                                                                                                                                                                                  DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGKQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                                                                                                                                                                                                                            AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                                                      IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240
                                                                                                                                                     VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                              IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKAWGKWYVNTTNIDGFRLDAVKHIK 274
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Borchert, Torben Vedel
Svendsen, Allan
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US-08-343-804-6
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Best Local S
Matches 514
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GENERAL INFORMATION:
APPLICANT: Bisgaan
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-MOV1994
CLASSIFICATION: 435
CCLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boröhert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
                                                                                                                                                                                                                                                        LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                      Similarity
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                                                                 DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                    AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
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VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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Borchert, Torben Vedel
Svendsen, Allan
                                                                                                                                                                        Conservative
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                                                                                                                                                                                   100.0%;
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                                                                                                                                                                    Score 2847; DB 2;
Pred. No. 1.7e-245;
); Mismatches 0;
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                                                                                                                                                                                                     Length 549;
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patent No. 5928381
GENERAL INFORMATION:
APPLICANT: Toft, A.
APPLICANT: Marcher
APPLICANT: Marcher
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US-08-687-399-6
                                                        , MOLECULE TO US-08-687-399-6
Query Match
Best Local Similarity
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIAN Release #1.0, \
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMBER: US/08/687,399
FILING DATE:
CLASSIFICATION: 008
ATTORNEY/ACENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4127.204
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marcher, Dorthe
APPLICANT: Pedersen, Hanne H.
APPLICANT: Nilsson, Thomas E.
TITLE OF INVENTION: A Combined Desizing and Bleaching
TITLE OF INVENTION: Process
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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                                                                             TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 Lexington Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 59283810 No. 5928381disk of No.
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  100.0%;
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    Score
Pred.
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    2847; DB 2;
No. 1.7e-245;
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Matches

514;

Conservative

0

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59891690 No. 5989169di.
STREET: 405 Lexington Avenue, 64th Fl
                                                                 REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-908A-6
                                                                                                                                                                                                                                                                 PATENILAG. 6022724

PATENILAG. 6022724

APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITILE OF INVENTION: '-Amylase Mutante
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vt CURRENT APPLICATION NUMBER: ITC/~~
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local Similarity
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CITY: New York
STATE: New Yor
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                                                                                                                                                                COUNTRY: United ZIP: 10174-6401
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                                                                                                                                                                                   New York
1: United States of
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100.0%; Pred. No. 1.7e-245;
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                                   US/08/683,838A
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                                                                          Version
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RESULT 12 US-08-600-908A-6

Sequence 6, Application US/08600908A Patent No. 5989169

GENERAL INFORMATION:

COUNTRY:

United States

of America

New York

10174-6401

TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:

TELEPHONE:

212-867-0123

ATTORNEY/AGENT INFORMATION: NAME: Green, Reza

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481

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RESULT 14
US-09-636-252A-6
Sequence 6, Application US/09636252A
Sequence 6, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILLING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
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SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/600,908
APPLICATION:
13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-U
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TYPE: amino acid
TOPOLOGY: linear
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Best Local S
Matches 514
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows
SEQ ID NO 6
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ORGANISM: B.
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nes 514; Conserv
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                      481 VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514
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                                                                                      GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
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                                                                 GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
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US-09-381-687-7

Sequence 7, Application US/09381687

Patent NO. 6486113

GENERAL INFORMATION:

APPLICANT: HATADA, Yuji
APPLICANT: HATADA, Yuji
APPLICANT: TO, Susumu
APPLICANT: HAGHARA, Hiroshi
APPLICANT: HAGHARA, Miroshi
APPLICANT: ARAKI, Hiroyuki
APPLICANT: ARAKI, Hiroyuki
APPLICANT: OZAKI, Katsuya
TITLE OF INVENTION: MUTANT ALPHA-AWYLASES
FILE REFERENCE: 2173-0115P
CURRENT APPLICATION NUMBER: US/09/381,687
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 7
LENGTH: 515
TYPE: PRT
CRGANISM: B. stearothermophilus
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Query Match  98.5%; Score 2005; Db 4; Length 515;  Best Local Similarity 98.8%; Fred. No. 8.9e-242;  Matches 508; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  1 AAPENGTMNQYFEWYLPDDGTLWTXVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY 60  1 AAPENGTMNQYFEWYLPDDGTLWTXVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY 60  1 AAPENGTMNQYFEWYLPDGTLWTXVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY 60  1 AAPENGTMNQYFEWYLPDGTLWTXVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY 60  2 61 DLYDLGEFNQKGTVRTKYGTXAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 120  2 61 DLYDLGEFNQKGTVRTKYGTXAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 120  2 7 121 VNPSDRNQEISGTYQIQAWTKFDFPGGRGNTYSSFKWRWHFPDGVDWDESRKLSRIYKFRG 180  2 121 VNPSDRNQEISGTYQIQAWTKFDFPGGRGNTYSSFKWRWYHFPDGVDWDESRKLSRIYKFRG 180  2 121 VNPSDRNQEISGTYQIQAWTKFDFPGGRGNTYSSFKWRWYHFPDGVDWDESRKLSRIYKFRG 180  3 1 1 IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240  3 1 1 IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240  3 2 2 4 1 FSFFPDWLSYVRSQTGXFLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300  3 2 4 1 FSFFPDWLSYVRSQTGXFLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300  3 3 1 SGGAFDMSTLMNNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG 360  3 0 1 SGGAFDMSTLMNNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG 360  3 0 1 SGGAFDMSTLMNNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG 360  3 0 1 SGGAFDMSTLMNNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG 360  3 1 1 YPCYFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420  4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Search completed: May 3, 2004, 20:35:57 Job time: 18.4001 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

15: /cgn2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

17: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

19: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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2847
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Match Length DB
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US-10-644-187-6
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                                                                                                                            Query Match 100.0%; Score 2847; DB 12; Length 514; Best Local Similarity 100.0%; Pred. No. 5e-256; Matches 514; Conservative 0; Mismatches 0; Indels 0;
                                          AAPFNGTMMQYFEWYLFDDGTLWTKVANEANNLSSLGITALWLFPAYKGTSRSDVGYGVY 60
   AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGTTALWLPPAYKGTSRSDVGYGVV 60
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1	2847	100.0	514	12	2 US-10-644-187-6	Sequence 6, Appli
2	2847	100.0	514	14	US-10-186-042-6	Sequence 6, Appli
w	2847	100.0	515	ø	US-09-854-346-6	Sequence 6, Appli
4	2847	100.0	515	9	US-09-918-543-6	Sequence 6, Appli
տ	2847	100.0	515	10	US-09-925-576C-6	Sequence 6, Appli
9	2847	100.0	515	14	US-10-146-327-8	Sequence 8, Appli
7	2847	100.0	549	14	US-10-184-771-6	Sequence 6, Appli
80	2829	99.4	549	14	US-10-081-872-104	Sequence 104, App
Q	2829	99.4	549	15	US-10-385-305-104	Sequence 104, App
10	2825	99.2	549	14	US-10-081-872-92	Sequence 92, Appl
11	2825	99.2	549	15	US-10-385-305-92	Sequence 92, Appl
12	2780	97.6	514	9	US-09-769-864-3	Sequence 3, Appli
13	2780	97.6	514	Ø	US-09-902-188A-3	Sequence 3, Appli
14	2780	97.6	514	12	US-10-665-667-3	Sequence 3, Appli

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ALIGNMENTS.		US-10-385-305-1 US-10-385-305-1 US-10-385-305-1 S-09-986-676A-2 S-09-971-611-2 S-09-769-864-1 S-09-769-864-7 S-09-854-346-2	10-327-837-3 9-795-211-4 10-081-872-10 10-385-305-10 10-081-872-88 10-105-733-7 10-385-305-88 10-081-872-13 10-385-305-12 10-385-305-12
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Sequence 6, Application US/10644187

Sequence 6, Application US/10644187

Publication No. US20040048351A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Bisgard-Frantzen, Henrik

APPLICANTON NUMBER: US/10/644,187

CURRENT FILING DATE: 1996-05

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6
; TYPE: PRT ; CRGANISM: Bacillus stearothermophilus US-10-644-187-6
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Sequence 6, Application US/10186042

Publication No. US20030171236A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Borchert, Torben

APPLICANT: APPLICATION NUMBER: US/10/186,042

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/9/672,459

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR APPLICATION NUMBER: 0515/96

PRIOR FILING DATE: 1996-04-30

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 37

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6

LENGTH: 514

Type: PAT

ORGANISM: Bacillus stearothermophilus

US-10-186-042-6
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US-10-186-042-6
                                                                    Query Match 100.0%; Score 2847; DB 14; Length Best Local Similarity 100.0%; Pred. No. 5e-256; Matches 514; Conservative 0; Mismatches 0; Indels
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         YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
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; Sequence 6, Application US/09854346
; Patent No. US202006835ZA1
; GENERAL INFORMATION:
APPLICANT: No. US2002006835ZA1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6
FILE REFERENCE: 6140.200.US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO
; LENGTH: 515
TYPE: PAT
ORGANISM: Bacillus stearothermophilus
US-09-854-346-6
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US-09-854-346-6
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IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240
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                                                                          VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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                                                       VMPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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US-09-918-543-6

Sequence 6, Application US/09918543

Patent No. US20020155574A1

GENERAL INFORMATION:
APPLICANT: Thisted, Thomas
APPLICANT: Moisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Kjaerulff, Soren
APPLICANT: Fuglang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
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Publication No. US20030129718A1

GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
ITITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRI
ORGANISM: Bacillus stearothermophilus
US-09-925-576C-6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andersen Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT APPLICATION NUMBER: US/09/537,168
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus Stearothermophilus
US-10-146-327-8
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                                                                                                                                       US-10-081-872-104
APPLICANT: Callen, Walter APPLICANT: Richardson, Tob APPLICANT: Frey, Gerhard APPLICANT: Short, Jay M. APPLICANT: Mathur, Eric J. APPLICANT: Gray, Kevin A.
                                                                                          GENERAL INFORMATION:
                                                                                                       Sequence 104, Application US/10081872 Publication No. US20030125534A1
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Short, Jay M.
Mathur, Eric J.
Gray, Kevin A.
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RESULT 7 US-10-184-771-6 ; Sequence 6, Application US/10184771 ; Publication No. US20030170769A1

Kerovuo, Janne

Toby

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GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Beigard-Frantzen, Henrik

APPLICANT: Berchert, Torben Vedel

ITITLE OF INVENTION: Alpha-Amylase Mutants

ITITLE OF INVENTION NUMBER: US/10/184,771

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/09/636,252

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 1996-07-18

PRIOR FILING DATE: 1996-07-18

PRIOR FILING DATE: 1996-07-18

INMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6

LENGTH: 549

TYPE: PRT

ORGANISM: B. stearothermophilus

US-10-184-771-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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                           VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514
                                                                                                                             GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLIGNRSDIVTINSDGWGEFKVNGGSVSVW
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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 548
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PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRT
ORGANISM: Environmental
US-10-081-872-104
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US-10-385-305-104
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Best Local Simi
Matches 511;
                                                Sequence 104, Application US/10385305
Publication No. US20040018607A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
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TITLE OF INVENTION: ENZYMES HAVING ALPHA ANYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
 APPLICANT:
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                              Richardson, Toby
Frey, Gerhard
Short, Jay M.
Mathur, Eric J.
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               Mathur, Eric J
Gray, Kevin A.
Kerovuo, Janne S
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Pred. No. 2.6e-254;
2; Mismatches 1;
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RESULT 10 US-10-081-872-92

Sequence 92, Application US/10081872
Publication No. US20030125534A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard

APPLICANT:

Richardson, Toby Frey, Gerhard Short, Jay M. Mathur, Eric J.

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APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-108001
CURRENT EPLICATION NUMBER: US/10/385,305
CURRENT EPLICATION NUMBER: US/10/081,872
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR PILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SCOTUMARE: FAST SEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRI
TYPE: PRI
TYPE: PRI
TYPE: PRI
TYPE: BRI
US-10-385-305-104
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Best Local Similarity, 99.4%;
Matches 511; Conservative
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                         VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
                                                                                              GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                                                                                YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
                                                                      ĠŚĠĿAALITDGPĠĠŚKWMYVĠKQHAĠKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2829; DB 15;
Pred. No. 2.6e-254;
2; Mismatches 1;
                                   514
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APPLICANT: Kerovio, Janne S.
APPLICANT: Slupaka, Malgorzata
FITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEO ID NOS: 321
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
TYPE: DET
Sequence 92, Application US/10385305
Publication No. US20040018607A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
                                                                                                           RESULT 11
US-10-385-305-92
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Pred. No. 6.1e
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US-09-769-864-3
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; TYPE: PRT
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Matches 511
  Sequence 3, Application US/097/
Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
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11; Conservative
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1; Mismatches
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APPLICANT: Gray, Kevin A.

APPLICANT: Kerovuo, Janne S.

APPLICANT: Silpska, Malgorzata

ITILE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY

TITLE OF INVENTION: AND METHODS OF USE THEREOF

FILE REFERENCE: 09010-108001

CURRENT FILLING DATE: 2003-03-06

PRIOR APPLICATION NUMBER: US/10/385,305

CURRENT FILLING DATE: 2002-02-21

PRIOR FILLING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/270,495

PRIOR APPLICATION NUMBER: US 60/270,496

PRIOR APPLICATION NUMBER: US 60/270,496
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APPLICANT: Nielsen, Bjarne
APPLICANT: Niesen, Torben L.
APPLICANT: Kjaerulff, Socen
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5366.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER: OF SEC ID NOS: 58
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
                                                                                                                         RESULT 13
US-09-902-188A-3
; Sequence 3, Application US/09902188A
; Patent No. US20020098996A1
; GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
Svendsen, Allan
Svendsen, Allan
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Best Local S
Matches 504
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: NO. US20020098996Alo No. US20020098996Aldisk
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
                                                                                                     Svendsen, Allan
Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-902-188A-3
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APPLICATION NUMBER: 09/354,191
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELEPHONE: 212.867 0123
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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,188A
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 514 amino acids
TYPE: amino acid
                                                                                                                                                            GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW 480
                                                                                                                                                                                                                                  YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
                                                                                                                                                                                                                                                                                                               SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG 360
                                                                                                                                                                                                                                                                                                                                                                                      FSFFFDMLSYVRSQTGKFLFTVGEYWSYDINKLHNYITKTDGTMSLFDAFLHNKFYTASK 300
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                                                                                             VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514
                                                                                                                                                                                                            YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKP
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                                                            VPRKTTVSTIAWSITTRPWTDEFVRWTEPRLVAW
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98.1%;
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Pred. No. 8.6e-250;
2; Mismatches 8;
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RESULT

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Sequence 3, Application US/1066567

Publication No. US20040038368A1

GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjærulff, Scren
ITILE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT FILING DATE: 2003-09-19
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/769,864
PRIOR APPLICATION NUMBER: US/09/769,864
PRIOR FILING DATE: 1998-10-30

NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 514
                                                                                     RESULT 15
US-10-025-648-3
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Sequence 3, Application US/10025648
Publication No. US20030064908A1
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Pred. No. 8.6e-250;
2; Mismatches 8;
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TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-025-648-3
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MEDIUM TYPE Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA: Release #1.0, Version #1.

APPLICATION NUMBER: US/10/025,648
FILING DATE: 19-Dec-2001

CLASSIFICATION NUMBER: 08/600,656
FILING DATE: 19-Dec-2001

PRIOR APPLICATION UNMBER: 08/600,656
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.1%;
Matches 504; Conservative
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Borchert, Torben Vedel
BORCHORT, Torben Vedel
NUMBER OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: NOVO Nordisk of North America,
ADDRESSEE: 405 Lexington Avenue, Suite 6400
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STATE: New York
COUNTRY: U.S.A.
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       GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGBFKVNGGSVSVW
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pred. No. 8.6e-250;
2; Mismatches 8;
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Search Job tir	DЬ	γĢ	дь
Search completed: May 3, 2004, 20:47:47 Job time : 41.0203 secs	481 VPRKTTVSTIAWSITTRPWIDEFVRWTEPRLVAW 514	481 VPRKTTVSTIARPITTRPWTGSEVRWTEPRLVAW 514	421 GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW 480

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Result
No.
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Maximum Match 100%
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2720.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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2847
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<b>.4</b>	44	43	42	41	40	39	38	37	36	ယ Մ	კ 4	ω ω	32	ω H	30
271.5	272.5	272.5	273	274.5	274.5	275.5	277.5	278	279.5	280	282	283	284.5	286	286.5
9.5	9.6	9.6	9.6	9.6	9.6	9.7	9.7	9.8	9.8	9.8	9.9	9.9	10.0	10.0	10.1
437	434	428	710	528	438	564	439	718	504	413	718	421	713	718	712
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S14956	S12775	S10013	S63598	ALBSK	S14957	T41503	T02956	ALBSGC	A55861	ALWT3	ALBSG6	S10514	ALBSG1	ALBSMX	ALBSG3
alpha-amylase (Ec	alpha-amylase (EC		cyclomaltodextrin	alpha-amylase (EC			alpha-amylase (EC	٠,	alpha-amylase (EC		- 5	alpha-amylase (EC		cyclomatcodextrin	cyclomaltodextrin

## ALIGNMENTS

Query Match Best Local Similarity 98.8%; Pred. No. 66-1 Best Local Similarity 98.8%; Pred. No. 66-1 Matches 508; Conservative 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLS 1	A;Start codon: GTG  C;Function: A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Description: calpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacd F;1-34/Domain: signal sequence #status predicted cSIG> F;235-349/Product: alpha-amylase status predicted cMAT> F;235-368/Domain: alpha-amylase core homology cAMY> F;139,237,272/Binding site: calcium (Asp. Asp. His) #status predicted F;268.298.365/Active site: Asp. Glu. Asp. #status predicted	A; Molecule type: DNA A; Residues: 1-549 <gra- 104.="" 105.="" 139501="" 170,="" 799="" a;="" alpha-amylase="" and="" bacteriol.="" been="" c:genetics:<="" c;="" copies="" cross="" cross-references:="" ddbj="" distal="" dy-5="" embl="" evidence="" experimental="" facession:="" fittle:="" focusion:="" for="" found="" from="" gb="" gb:m13255;="" gb:m29577;="" gb:m29578;="" gene="" genes="" genetics:="" gomment:="" h.="" h.;="" have="" in="" into="" isono,="" j.="" j9501="" k.="" movement="" multiple="" nid:g142476;="" nid:g142484;="" nid:g142512;="" nishida,="" of="" on="" phylogenetically="" pid:g142478="" pid:g142486="" pid:g142513="" pidn:aaa22225.1;="" pidn:aaa22228.1;="" pidn:aaa22241.1;="" plasmids="" preliminary;="" references:="" satch,="" source:="" status:="" strain="" th="" the="" title:="" translated="" two=""><th>275 FSF 301 SGC 301 SGC 301 YPC 305 YPC 307 YPC 307 YPC 307 YPC 307 YPC 421 GSC 421 GS</th></gra->	275 FSF 301 SGC 301 SGC 301 YPC 305 YPC 307 YPC 307 YPC 307 YPC 307 YPC 421 GSC 421 GS
	: 139777 reliminary; translated from GB/EMBL/DDBJ reliminary; type: DNA 1-45 <res> 6-45 <res> 6-45 <res> Alpha-amylase genes have been found on plasmids and in multiple 7-8 7-8 7-8 7-8 7-8 7-8 7-8 7-8 7-8 7-8</res></res></res>	RESULT 3  A24436 alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5 alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5 N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus stearothermophilus C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999 C;Accession: A24436; I39777 R;Nakajima, R.; Imanaka, T.; Alba, S. J. Bacteriol. 163, 401-406, 1985 J. Bacteriol. 163, 401-406, 1985 A;Reference number: A24436; MUID:85234394; PMID:3924897 A;Reference number: A24436 A;Molecule type: DNA A;Residues: 1-594 <nnac 139772;="" a="" a;cross-perence="" a;cross-references:="" a;reference="" a;title:="" as="" cons="" engineering:="" for="" gb:m11450="" genetic="" homologous="" in="" j990="" muid:91094499;="" number:="" plasmid="" pmid:2265757<="" recombination="" td="" tool="" vivo=""><td>Qy 61 DLYDLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 120 bb 95 DLYDLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 154 Qy 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNIYSSFKWWWHFDGVDWDESRKLSRIYKERG 180 [                                    </td></nnac>	Qy 61 DLYDLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 120 bb 95 DLYDLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE 154 Qy 121 VNPSDRNQEISGTYQIQAWTKFDFPGRGNIYSSFKWWWHFDGVDWDESRKLSRIYKERG 180 [

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RESULT 4
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Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain D alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain D N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus stearothermophilus C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 16-Feb-1997 C;Accession: A91999; B91999; A91804; A00845
R;Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S.
J. Biochem. 98, 95-103, 1985
A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: A;Reference number: A91999; MUID:86008166; PMID:3876333
A;Accession: A91999
                                                                                                                                              A; Molecule type: protein
A; Residues: 35.48 <1H2>
A; Experimental source: strain DY-5
R; Tsukagoshi, N.; Iritani, S.; Sasaki, T.;
J. Bacteriol. 164, 1182-1187, 1985
A; Title: Efficient synthesis and secretion
A; Reference number: A91804; MUID:86059211;
A; Contents: pBAM101
A;Accession: A91804
A;Accession: A91804
A;Accession: N91804
A;Molecule type: DNA
A;Molecule t
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A;Residues: 1-548 <IH1>
A;Coss-references: GB:X02769
A;Experimental source: plasmid
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A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core hc C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core hc C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrol F;134/Domain: signal sequence #status predicted <SIG
F;134/Domain: alpha-amylase #status experimental <MAT>F;35-548/Product: alpha-amylase core homology <AMY>F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted F;268,298,365/Active site: Asp, Glu, Asp #status predicted
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                      VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
                                                                                                                       GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                                                                                                                  YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
VPRKTTVSTIARPITTRPWTGEFVRWHEPRLVAW
                                                                                 GSGLAAL ITDGAGRSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
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96.7%;
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alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence\_revision 18-Aug-1995 #text\_change 18C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A;Title: Nucleotide sequence of the maltohexaose-producing amylase
A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705 A;Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g142497
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from thi
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A; Molecule type: DNA A; Residues: 1-518 < TSU>

18-Jun-1999

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this organism

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A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degrada'
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-518/Product: alpha-amylase #status experimental <MAT>
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               A; Molecule type: DNA
A; Restdues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A; Cross-references: GB: MI3256; NID: g142510; PIDN: AAA22240.1;
A; Experimental source: NCIB_8061
                                                                                                               A;Molecule type: DNA
A;Residues: 1-162,'R',164-512 <YUU>
A;Residues: 1-162,'R',164-512 <YUU>
A;Residues: 1-162,'R',164-512 <YUU>
A;Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
A;Experimental source: ATCC 27811
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.;
G. Bacteriol. 166, 635-643, 1986
A;Bacteriol. 166, 635-643, 1986
A;Tille: Structural genes encoding the thermophilic alpha-amylases of Bacillus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus licheniformis C;Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text_change 15-Sep-2000 C;Date: 30-Jun-1997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844 C;Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844 R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka D; Blochem. 98, 1147-1156; 1985
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                                                                                                                                                                                                                                                                                                                                            A;Title: Complete nucleotide sequence of a ases deduced from the DNA sequences. A;Reference number: A91997; MUID:86111694; A;Accession: A91997
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A;Note: sequence represents amino end of an internal fragment cres R;Machius, M.; Wiegand, G.; Huber, R. submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A65206; PDB:1BPL
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, resi A;Note: these structural studies suggest 163 is Leu rather than Ar R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W. submitted to the Brookhaven Protein Data Bank, October 1996
A;Reference number: A66860; PDB:1VJS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, resi C;Genetics:
A;Gene: amyL
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A,Reference number: A91796; MUID:84185455; PMID:6609154
A,Recession: A91796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 30-37,'E',39-41,'X',43-47 <KUH>
R;Residues: 30-37,'E',39-41,'X',43-47 <KUH>
T,Mol. Biol. 246, 545-559, 1995
J. Mol. Biol. 246, 545-559, 1995
A;Title: Crystal structure of calcium-depleted Bacillus
A;Reference number: S53788; MUID:95182462; PMID:7877175
A;Accession: S53788
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A;Title: In vivo genetic engineering: homol
A;Reference number: I39772; MUID:91092499;
A;Accession: I39772
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A;Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1;
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen,
Gene 96, 37-41, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 171, 2435-2442, 1989
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, A;Reference number: I39773; MUID:89213924; PMID:2540150
A;Accession: I39774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S' A;Experimental source: chromosomal DNA of ATCC 14580 A;Note: the authors translated the codon CGT for residue 48 as Gly and GAC f. R;Laoide, B.M.; Chambliss, G.H.; McConnell, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 145, 567-572, 1984
A; Title: Isolation and the 5'-end nucleotide sequence of A; Reference number: A21663; MUID:85076654; PMID:6334606
J. Bacteriol. 149, 372-373, 1982
A,Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase:
A,Reference number: A26151; MUID:82098050; PMID:6172418
A;Accession: A26151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O. J. Bacteriol. 149, 372-373, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
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A;Residues: 'D',220-227 <MAC>
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A; Residues: 1-32,'I'
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Query Match Best Local

Local Similarity

Score Pred.

No. 5.6e

5; DB 1; .6e-122;

Length

site: Asp, Glu, 63.0%; Sc ity 65.0%; Pr

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RESULT 7
ALBSN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amyloliquefaciens
C;Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A93389; A93307; I39756; I39763; A00843
R;Takkinen, K; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced f A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: pUBl10
****Pracesion** A92389
                                                                                                             A;Molecule type: protein
A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
A;Residues: 1, Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas,
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal
A;Reference number: 139756; MUID:82051296; PMID:6170539
A;Accession: 139756
                                                                                                                                                                                                                                         A;Cross-references: GB:J01542; GB:J01543; GB:M12034; NID:g14
R;Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
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A;Molecule type: DNA
A;Residues: 1-514 <TAK>
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;Cross-references: EMBL:V00092; NID:g39297;
;Ruohonen, L.; Hackman, P.; Lehtovaara, P.;
ene 59, 161-170, 1987
                                                         ;Molecule type: DNA
;Residues: 1-96 <RES>
                                                                                           Status: translated from
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                                                                                             GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                    GB:J01543; GB:M12033; GB:M12034; NID:g142428;
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                   PIDN:CAA23430.1;
Knowles, J.K.C.;
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                   PID:g39298
Karaenen, S.
                                                                                                                                                                                       Sarvas,
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A;Status: preliminary
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A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase ce A;Reference number: 139763; MUID:88137952; PMID:2830166
A;Recession: 139763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-39 <RE2-
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C;Function:
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degrada
F;1-31/Domain: signal sequence #status predicted <810>
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Best Local
512
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                                                                                                           GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                                                                              FDMRTLMTNTLMKDQFTLAVTFVDNHDTEFGQALQSWVDFWFKFLAYAFILTRQEGYPCV
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VQK 514
                                                                                      KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                                                                                                                                                                                                                                                                                                                                 PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA
                                           VPR 483
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; Pred. No. 1.8e-120;
57; Mismatches 105;
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strain PCC :

alpha-amylase [imported] - Nostoc sp. (strain PCC 7120) c/Species: Nostoc sp. PCC 7120 a./Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. A;Note: 14-bec-2001 #sequence\_revision 14-bec-2001 #text\_change c/pate: 14-bec-2001 #sequence\_revision 14-bec-2001 #text\_change c/Accession: AH2079 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M. DNA Res. 8, 205-213, 2001 DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2079 , s., v Watanabe, Yasuda, Cyanobacterium 3 Α., Iriguchi ß

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RESULT 9
alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
c.Species: Streptococcus pneumoniae
c.Species: Streptococcus pneumoniae
c.Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
c;Accession: d95160
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
A;Anthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Anthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Accession: G95160
A.;Status: preliminary
A;Accession: G95160
A.;Status: preliminary
A;Cross-references: GB:AB005672; pIDN:AAX75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: Sp1382
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-492 <KUR>
A;Residues: 1-492 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73889.1; PID:g17131281; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a122190
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homolo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDE--SRKLSRIYKF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEFKVNGGSVSVWV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIGWTREGGTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGW
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alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6) c)Species: Streptococcus pneumoniae (c)Species: Streptococcus pneumoniae (c)Species: Streptococcus pneumoniae (c)Species: Streptococcus pneumoniae (c)Species: 22-Oct-2001 #text_change 02-Nov-2001 C)Accession: F98026 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N. Y. P.; Sun, P.M.; Winkler, M.E. J.; Bacteriol. 183, 5709-5717, 2001 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: F98026 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-484 <KUR> A;Genetics: GB:AE007317; PIDN:AAL00043.1; PID:g15458876; GSPDB:GN00174 C;Genetics: GB:AE007317; PIDN:AAL00043.1; PID:g15458876; GSPDB:GN00174
                                                                                                                                                      A;Gene:
C;Superf
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                                                                                                                                                  Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase;Keywords: glycosidase; hydrolase
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                                                                                        Similarity
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                                                                   Score 1311; DB 2;
Pred. No. 4.5e-87;
74; Mismatches 158;
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3; Mismatches 158
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RESULT 11

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Sipha-amylase (EC 3.2.1.1) - Bacillus circulans
C;Species: Bacillus circulans
C;Species: Bacillus circulans
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: $15713
R;Marcel, T.
submitted to the EMBL Data Library, May 1991
A;Reference number: $15713
A;Accession: $1571
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                                WDWEYDTENGNYDYLMYADLDMDHPEVVTBLKNWGKWYVNTTNIDGFRLDAVKHIKFSFF
                                                                                                                                                                                       LGEFDQKGTVRTKYGTKQELIEAIAECQKNGIAVYVDLVMNHKAGADETEVFKVIEVDPN
                                                                                                                                                                                                                                LGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVFYGDYYGISGQYAQQDFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAENQ--
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                                                                                             DRTKEISEPFEIEGWTKFTFPGRGDQYSSFKWNSEHFNGTDFDAREERTGVFRIAGENKK
                                                                                                                                     DRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA 184
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WNENVDDEFGNYDYLMFANIDYNHPDVRREMIDWGKWLIDTLQCGGFRLDAIKHINHEFI
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Pred. No. 1e-84;
4; Mismatches 1
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A;Molecule type: DNA
A;Residues: 1-491 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: C86781
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                                          AALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRK 484
                                                                                                                                FYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKPGSGL
                                                                                                                                                                                                                                                                                                                        PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA 304
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  SCILTNKNGGSKYMIIDKAYAGKVYIDLFGRHEIPITLDQNGGAEFYVNDGSVSVWVD-K
                                                                                   FWGDLYGIPSHNVNPVGDNLRTMIALKKÖSEFLRENDYPDHPDIIGWTNILKIDNKEYGL
                                                                                                                                                                                       FDMRTLFDHTLTASQPELSVTFVDNHDTQEGQALQSWIPAWFKEHAYSLILLRKKETPTV
                                                                                                                                                                                                                                POMRTLMINITAMOPTIAVTEVDHIDTEPGOALOPWOVEKPLAYAFILTROEGYPCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.2%; Score 1229; DB 2; llarity 47.5%; Pred. No. 3.8e-81; Conservative 73; Mismatches 176;
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Length alpha-amylase

core

homology

GSPDB:GN00146

(strain

IL1403)

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K.; Weissenbach, 03-Aug-2001

J.; Ehrli lactis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 174, 6644-6652, 1992
A; Title: Escherichia coli produces a cytoplasmic alpha-amylase,
A; Reference number: A45738; MUID:93015717; PMID:1400215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium N;Alternate names: 1,4-alpha-plucan glucanohydrolase C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999 C;Accession: B45/38
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A; Residues: 1-494 < RAH>
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                                       KVNGGSVSVWV 481
                                                                                                                                                      PSVFYPDLYGASYEDSGENGETCRVDMPVI-NQLDRLILARQRFAHGIQTLFFDHNNCIA
                                                                                                                                                                                                                                                                                  GGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGY 361
                                                                                                                                                                                                                                                                                                                            WFYKEWIEHVQAVAPKPLFIVAEYWSHEVDKLQTYIDQVDGKTMLFDAPLQMKFHEASRQ 302
                                                                                                                                                                                                                                                                                                                                                               SEEPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKS
                                                                                                                                                                                                                                                                                                                                                                                                      GDGWNDQVDDEMGNFDYLMGENIDFRNHAVTEBIKYWARWVMEQTHCDGFRLDAVKHIPA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                               GKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDRTQIDDNI IECEGWTRYTFFARAGQYSNFIWDYHCFSGIDHIENPDEDGIFKI VNDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDRNQEISGTYQIQAWTKFDFFGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG--I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIGEFDOXGTIATKYGDKROLLTAIDALKKUNIAVLLDVVVNHKMGADEKERIRVQRVNQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPTILLQYFHWYYPDGGKLWSELAERADGLNDIGINMVWLPPACKGASGGYSVGYDTYDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRS-DVGYGVYDLY
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                                                                            FSRSGTEENP--GCVVVLSNGDDGEKTLLLGDNYANKTWRDFSGNRDEYVVTNDQGEATF
                                                                                                                   WTREGGTERPGSGLAALITDGPGGSKWMYVGRQHAGKVFYDLTGNRSDTVTINSDGWGEF
                                                                                                                                                                                                    PCVFYGDYYGIP----
                                                                                                                                                                                                                                             GAEYDMRHIFTGTLVEAD FHAVTLVANHDTQPLQALEAPVEPWFKPLAYALILLRENGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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44.0%; Pred. No. 1e-72;
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    Salmonella typhimurium glucanohydrolase

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RESULT AD0751

14

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002
C;Accession: AD3038
C;Accession: AD3038
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chenerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.

Wood, G.E.; Chen, T.; Levy, R.; Li,

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McClella

alpha-amylase amyA [imported] - Agrobacterium tumefaciens  $C_\ell$ Species: Agrobacterium tumefaciens

(strain C58,

science 294, 2317-2323,

Biddle,

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Jung,

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Krespan,

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Perry,

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Gordon-Kamm,

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A;Cross-references: C;Genetics:
A;Gene: STY2171
C;Superfamily: alpha-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608 A;Accession: AD0751
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A;Molecule type: DNA
A;Residues: 1-494 <PAR>
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Best Local Similarity
Matches 216; Conserv
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S.; O'Gaora, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG--I 181
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                                                                                                                                                                                                                                                                                                                                                                 SFFPDWLSYVRSQTGKPLFTYGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRTQIDDNIIECEGWTRYTFFARAGQYSNFIWDYHCFSGIDHIENPDEDGIFKIVNDYT 182
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                                     KVNGGSVSVWV 481
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FCNAGSVSVWV
                                                                                                                    WIREGGIEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVIINSDGWGEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.7%; Score 1101.5; DB 2;
44.0%; Pred. No. 6.3e-72;
tive 82; Mismatches 176;
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ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Croos-references: GB:AE08689; PIDN:AAL44722.1; PID:gl7742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
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481
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                                                                                    423 IRHGTADAP--GCVVVMSNGEPGEKQADLGPERAGSVWRDFLGHREEHITLDESGKGTFP 480
                                                                                                            412 TREGGTEKPGSGLAALITDGPGGSKWMYYGKQHAGKVFYDLTGNRSDTVTINSDGWGEFK 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEFDQKGTVATKYGDRAALEHAGKTLKDNGIRVIHDVVLNHKMGADEKEKVRVRRVNPDD 124
TNGGSVSVWVP 491
                                   VNGGSVSVWVP 482
                                                                                                                                                                CVFYPDLEGTSYTDTGNDGNEYKIDIPAIEC-LEKLIEARSRFANGPQTDIFDDASCIAF
                                                                                                                                                                                                                 CVFYGDYYGIP------OYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSBIIGW 411
                                                                                                                                                                                                                                                              GDFDMRSIFDGSLVSAVPDHAVTLVDNHDTQPLQSLEAPVEPWFKPLAYAIILLREEGVP
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Search completed: May 3, 2004, 20:54:07 Job time: 15.6161 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                               SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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(without alignments)
4438.289 Million cell updates/sec
     US-10-644-187-6
2847
1 AAPENGTMMQYFEWYLPDDG.....TTRPWTGEFVRWTEPRLVAW 514
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Gapop 10.0 , Gapext 0.5
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                                                                                            sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_bacteriap:*
sp_bacteriap:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

esult No.	Score	% Query Match	% Query Match Length DB	DB	Ħ	Description
1	2833	99.5	549	ا ۵	031193	O31193 bacillus st
2	2811	98.7	549	ผ	Q9KWY6	
ω	2658	93.4	521	N	P71034	
4	2404	84.4	613	N	Q59222	
ហ	1910.5	67.1	516	N	082839	
თ	1841.5	64.7	533	N	Q9AQ54	bacillus
7	1837.5	64.5	519	N	Q9RQT8	Q9rqt8 cytophaga s
œ	1829.5	64.3	513	16	Q81AS4	Q81as4 bacillus ce
9	1827.5	64.2	513	16	Q81YJ4	Q81yj4 bacillus an
10	1700	59.7	507	16	Q87HG6	Q87hg6 vibrio para
11	1618	56.8	501	N	Q93I48	Q93i48 bacillus sp
12	1345.5	47.3	492	16	1ZUY8Q	Q8yuz1 anabaena sp
13	1322.5	46.5	481	16	147680	Q89yp1 bacteroides
14	1315	46.2	484	16	Q97Q49	Q97q49 streptococc
15	1311	46.0	484	16	QBDPCB	Q8dpc8 streptococc
<u>س</u>	1296	4 л	498	7	OMFOMO	ORPORO STREET OFFICE

片 Ş

A1 DI VDI CERNOKOTVATKVOTKAOVI DA TORAHA

35 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY 94

AGMOVYADVVFDHKGGADGTEWVDAVE 120

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Q94A41	Q9CAR6	Q8VZ56	Q8LBS5	Q8LQK4	Q60051	093647	Q8JZK3	Q9F9L0	· Q8U3I9	008452	033476	050200	Q8NKR4	Q8NKR5	Q877B1	Q83R40	Q7UAB0	Q8XBB6	Q8FGL8	Q8U916	Q8Z5S5	Q9CG59	068875	Q53786	050583	Q8DT08	Q03657	89
arabidopsi	Q9car6 arabidopsis	Q8vz56 arabidopsis	Q8lbs5 arabidopsis	Q8lqk4 oryza sativ	Q60051 thermoactin	093647 thermococcu	Q8jzk3 uncultured	rococcus	Q8u3i9 pyrococcus	008452 pyrococcus	033476 pyrococcus	050200 thermococcu	Q8nkr4 thermococcu		_		0 shigella	escherichi	Q8fg18 escherichia	Q8u916 agrobacteri	85	59	80.0	9	B	80	Д	96 streptoco

## ALIGNMENTS

RESULT 1

DR PIR;	88						Mar Bes Bes Bes Bes Bes Bes Bes Bes Bes Bes
UMBI; AKUJAB64; AABB6961.1; UHD. 964641, NEJE41	HSSP; P06278; 1VJS.	US:I. F:alpha-amylase activity; I F:arrhohvdrate metabolism.	ty; ism	1VJS. ; F:alpha-amylase activity; I ; F:aspha-amylase activity; I ; F:carbohydrate metabolism; 06047; Alpha amyl cat. 06589; Alp amyl cat sub. 06046; Glyco hydro 13.	ty; I ism;	ty; I ism;	, P06278; IVJS.  , P06278; IVJS.  30:0005975; P:carbohydrate metabolism; IEA. rPro; IPR006047; Alpha_amylase activity; IEA. rPro; IPR006047; Alpha_amyl_cat. rPro; IPR006049; Alpha_amyl_cat_sub. rPro; IPR006049; Alp_amyl_cat_sub. rPro; IPR006049; Alpha_amylase; 1.  TS; PR00110; Alpha_amylase; 1.  TS; PR00110; Alpha_AMYLASE.  TI; SM00642; Aamy; 1.  ENCE 549 AA; 62651 MW; 2CA689EDACC4D262 atch Similarity 99.5%; Pred. No. 7.9e-186; 512; Conservative 1; Mismatches

514 480 454 360

394

240

214 180 154

300 274

334

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OSCAPACIONE DE CONTROL DE CONTROL
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                                                                                                                         Query Match 98.7%; Score 2811; DB 2; Length Best Local Similarity 99.0%; Pred. No. 2.5e-184; Matches 509; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                           Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databet EMBL; Y17557; CAB93517.1; -.

PIR; A54541; A54541.

HSSP; p06278; IVJS.

GO; GO:0016798; F:Alpha-amylase activity; IEA.

GO; GO:0016798; F:Alpha-amylase activity, acting on gly

GO; GO:0005975; P:Carbothydrate metabolism; IEA.

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006047; Alpha_amyl_cat sub.

InterPro; IPR00659; Alp amyl_cat sub.

InterPro; IPR006698; Alp amyl_cat.

INTERPRO; IPR006698; Alp amyl_cat.

INTERPRO; IPR0066946; GlyCo_hydro_I3.

PRINTS; PR001128; alpha-amylase; I.

PRINTS; PR00110; ALPHAMYLASE.

SMART; SM00642; Almy; 1.

GlyCosidase; Hydrolase.

SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRO
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Q9KWY6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
Bacillus stearothermophilus.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Geomorphilis
MCBI TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=US100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
DLYDLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
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                                                        AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                           AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
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Best Local S
Matches 480
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HSSP; P06278; IVUS.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0004556; F:alpha-amylase metabolism; IEA.
Interpro; IPR006047; Alpha-amylase;
Interpro; IPR0060889; Alp, amylast sub.
Interpro; IPR0060889; Alp, amylast sub.
Interpro; IPR006046; Glyco_hydro_T3.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAMYLASE.
PRINTS; PR001010; ALPHAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p71034 PRELIMINARY; PRT;
p71034;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 24, Last seq
01-UN-2003 (TrEMBLrel. 24, Last ann
Alpha-amylase precursor.
Bacillus sp. MK 716.
Bacteria; Firmicutes; Bacillales; Ba
                                                                                                                                                                                   PRINTS; P
SMART; SM
Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-MK 716;
STRAIN-MK 716;
Sidhu G.S., Chakarbarti T.;
Sidhu G.S., Chakarbarti T.;
"Molecular cloning and expression of the gene encoding for thermostable alpha-amylase of a thermophilic bacterial isolate.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBU databases.
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                                                                                                              tch 93.4%;
al Similarity 99.2%;
480; Conservative
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                                      VPRKTTVSTITRPITTRPWTGEFVRWTEPRLVAW
                                                                                                                                                                                     35
521 AA;
                                                                                                                                                                                 34 PC
521 AI
; 59311 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                22
                                                                                                                Score 2658; DB 2;
Pred. No. 7.1e-174;
2; Mismatches 2;
                                                                                                                                                                                                       POTENTIAL.
ALPHA-AMYLASE
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                                                                                                                                                                                         CRC64;
                                                                                                                                                 Length 521;
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43

DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE

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R HSSP; P06278; IVUS.

R GO; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:000647; F:hydrolase activity; IEA.

R GO; GO:000847; F:purine nucleosidase activity; IEA.

R GO; GO:000897; F:curine nucleosidase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

PR InterPro; IPR006647; Alpha amyl cat.

PR InterPro; IPR006689; Alp amyl cat.

R InterPro; IPR006689; Alp amyl cat.

R InterPro; IPR006044; CBD_4.

R InterPro; IPR006044; CBD_4.

R InterPro; IPR006046; Glyco hydro_13.

Pfam; PF00128; alpha-amylase; 1.

Pfam; PF00128; alpha-amylase; 1.

R PRINTS; PR00110; Alpha-AMYLASE.

R ProDom; PD001569; CBD_4; 1.

R ProDom; PD001569; CBD_4; 1.
                                                                                 Query Match
Best Local Similarity
Matches 432; Conserv
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O59227
O59222;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp. TS-23.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin L.-L., Chu W.S.,
Submitted (MAR-1995)
                                                                                                                                                                                                Glycosidase; Hydrolase
SEQUENCE 613 AA; 699
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APFNGTYMQYFEWYLPDDGTLWIKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPRR 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
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                                                                                       Conservative
                                                                                                                                                                                                   69537 MW; 14684A30FC2895E8 CRC64;
                                                                                                            84.4%;
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales;
                                                                                 31;
                                                                                    Score 2404; DB 2;
Pred. No. 2.2e-156;
1; Mismatches 50;
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                                                                                                                                       Length
                                                                                       Indels
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NGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD

Query Match
Best Local Similarity
Matches 329; Conserv

Conservative

69;

67.1%;

Score 1910.5; DB 2; Pred. No. 1.1e-122; 9; Mismatches 79;

Indels Length

1;

Gaps

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RESULT 5
O82839
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01-NOV-1998
01-NOV-1998
01-JUN-2003
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha-amyl_cat.
InterPro; IPR006048; Alpha-amyl_cat sub.
InterPro; IPR006046; Glyco_hydro_T3.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00107; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                     Ožaki K., Ito S.; "Improved thermostability of a Bacillus alpha-amylase by deletion of "Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding."; an arginine-glycine residue is caused by enhanced calcium binding."; Biochem. Biophys. Res. Commun. 248:372-377(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amylase.
Bacillus sp.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                082839
                                                                                                                                                                                                                                                       EMBL; AB008763; BAA32431.1; -. HSSP; P06278; 1VJS.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98342096; PubMed=9675143; Igarashi K., Hatada Y., Ikawa K.,
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24,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    Araki H., Ozawa
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Best Local S
Matches 317
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Q9AQ54;
01-JUN-2001
01-JUN-2001
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HSSP; P06278; IVJS.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alpha_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase.
Bacillus megaterium.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of maltopentaose-producing amylase from Bacillus megaterium KSM B-404.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Kim Y.B., Lee B.N., Park K.-H.;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPC
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DRNQEISGTYQIQAWTKFDFPGRGNTYSSFXWRWYHFDGVDWDESRKLSRIYKFRGIGKA
                                                                      LGEFNQKGTVRTKYGTKAQLKSAIDALHKKNIDVYGDVVMHKGGADYTETVTAVEVDPS
                                                                                                                                                           NGTLMQYFEWYAPNDGNHWNRLRTDAENLAQKGITSVWIPPAYKGTTQNDVGYGAYDLYD
                                                                                                                                                                                      NGTMMQYFEWYLPDDGTLWTXVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Son H.J., Lee
                                                                                                                                                                                                                                                                         64.7%; Score 1841.5; DB 2 65.8%; Fred. No. 6.2e-118;
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Best Local Similarity
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AF067653; AAF00567.1; --
HSSP; P06278; IVJS.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006649; Alpha_amyl_cat.
InterPro; IPR006649; Alpha_amyl_cat.
InterPro; IPR006046; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHANMYLASE.
SMART; SM00642; Aamy; 1.
SIGNAL
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SEQUENCE
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Bacteria; Bacteroidetes; Sphingobacteria;
Flexibacteraceae; Cytophaga.
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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       154
                                                   121
                                                                                              94
                                                                                                                                61 DLYDLGEENOKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                                                                      34
                                                                                                                                                                                                            1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGLAALITDGPGGSKMMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYGDYYGI---PQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDMRTLMINILMKDQPTLAVTEVDNHDTEFGQALQSWVDPWFKPLAYAFILIRQEGYPCV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDWVNHVRQQTGKEMFAVAEYWQNDİQTLNNYLAKVNYNQSVFDAPLHYNFHYASKGNGN
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                             VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                                                                                                    VNPSNRNOETSGEYNI OAWIGFNFPGRGTTYSNFKWQWFHFDGTDWDQSRSLSRIFKFRG
                                                                                              DLYDLGEFNQKGTVRTKYGTKGELKSAVNTLHSNGIQVYGDVVMNHKAGADYTENVTAVE
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519
                                                                                                                                                                                                                                                                              Conservative
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519 R
58337 MW;
                                                                                                                                                                                                                                                                         64.5%; Score 1837.5; DB 2
67.4%; Pred. No. 1.1e-117;
cive 57; Mismatches 98;
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13,
24,
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RAW STARCH DIGESTING AMYLASE,
3E6B88A4DF98B163 CRC64;
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Q81AS4;

Q81AS4;

Q81AS4;

O1-JUN-2003 (TrEMBLrel. 24, Created)

O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINB-22608415; PubMed=12721630;
MEDLINB-22608416, A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus
Kapatral V., Bhattecharyya A., Reznik G., Mikhailova N., Lapidus
Kapatral V., Bhattecharyya A., Larsen N., D'Souza M., Walunas T.
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.
Chu L., Mazur M., Goltsman E., Fonstein M., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                        Nature 423:87-91(2003).

EMBL; AE017009; AAP10417.1; -.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0004576; F:hydrolase activity, acting on glycosyl bonds;

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds;

GO; GO:005975; P:carbbhydrate metabolism; IEA.

InterPro; IPR00647; Alpha amyl_cat.

InterPro; IPR006589; Alp_amyl_cat_sub.

Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.

SMART; SM00642; Aamy; 1.

SMART; SM00642; Aamy; 1.

SMART; SM00642; Aydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grechkin Y., Pusch G., Haselkorn R.,
Overbeek R., Kyrpides N.;
"Genome sequence of Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=226900;
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315; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPCVFYGDYY---GIPQYNIPSLKSKIDPLLİARRDYAYGTQHDYLDHSDIIGWTREGGT
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                                                                                                                              NGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
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                                                                      DGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
DRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firmicutes;
                                                                                                                                                                                                                                                                                                       ; Hydrolase; Complete proteome.
513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                        64.3%;
                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                        Score 1829.5;
Pred. No. 3.96
                                                                                                                                                                                                                     Mismatches
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                                          YTETVTAVEVDPS
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                                                                                                                                                                                                                   Gaps
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Q81YJ4;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                       Complete
SEQUENCE
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Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Nelson K.E., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A
                                                                                                                                                                                                                                                           GO; GO:0004556; F:alpha-amylase activity; GO; GO:0005975; P:carbohydrate metabolism; InterPro; IPR006047; Alpha_amyl_cat. InterPro; IPR006589; Alp amyl_cat_sub. Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.
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AMYS OR BA3551.
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                                                                                                                                                                                                                                                                                                                                                                                                Nature 423:81-86(2003).
EMBL; AE017035; AAP27311.1;
TIGR; BA3551; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of Bacillus closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis (s
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYGDYYGTKGNSNYEIPALKDKIDPILTÁRKNFÁYGTÓRDYFDHPDVIGWTREGDSVHAN
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513 AA;
  LGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
                                                                        NGTMYQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
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llarity 65.8%;
Conservative 6
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es; Bacillales;
                                                                                                                                                                                                                     58445 MW;
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Last sequence up
Last annotation
                                                                                                                                   Score 1827.5; DB 16;
Pred. No. 5.3e-117;
59; Mismatches 92; 1
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Query Match
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Q87HG6;
01-JUN-2003
01-JUN-2003
01-OCT-2003
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MEDLINB=22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

EMBL; APP05087; BAC62342.1; -.
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VPA0999.
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                                                                                                                                                                                                                                                                                                                                                            GG; GO:0004556; F:alpha-amylase activity; IEA.
GG; GO:0005975; P:catoohydrate metabolism; IEA
InterPro; IPR006047; Alpha amyl cat.
Pfam; PF00128; alpha-amylase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDWVNHVRQQTGKEMFTVAEYWQNDIQTLNNYLAKVNYNQSVFDAFLHYNFHYASKGNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA 304
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                                                                                                                                                                                           NGTMMOYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRS-DVGYGVYDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLGEFDQKGSVRTKYGTKAQYISAINAAHNNNIQIYGDVVFNHRGGADGKSWVDTKRVDW
                                                                                                                                                  NGTMMQYFHWYVPNDGALWTQVESNAPALAENGFTALWLPPAYKGAGGSNDVGYGVDMY
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                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                          58428 MW; 91B549E2BE0700BD CRC64;
                                                                                                                                                                                                                                                          59.7%;
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Last annotation update)
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                                                                                                                                                                                                                                    Score 1700; DB 16;
Pred. No. 2.8e-108;
6; Mismatches 102;
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Q93148;
Q1-DEC-2001
01-DEC-2001
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of a new Bacillus alpha-amylase.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; AB051102; BAB71820.1; .
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00128;
SEQUENCE 501
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STRAIN=KSM-K38;
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Bacteria, Firmicutes;
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                                                                                     WDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFF
                                                                                                                                                       DRNQBISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDBSRKLSRIYKFRGIGKA
                                                                                                                                                                                                                                                                                                     NGTMMOYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
                                               WIWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIDFWYT
                                                                                                                                NRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQRYQENHIFRFANTN--
                                                                                                                                                                                                                    LGEFNOKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQVNPT
      PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA
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AA; 57485 MW;
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Pred. No. 1.2e-102;
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01-JUN-2003 (Tr
Alpha-amylase.
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SEQUENCE
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PRINTS; PR00110; ALPHAAMYLASE.
Complete proteome.
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30; GO:0005975; P:carbohydrate metabolism;
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_nydro_13.
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ISTWFFPEWIDALERHAGKDLFMVGEYWYNDINTLLWYVDAVRGKMSVFDVPLHYNFHQA
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shima K., Kimura T.,
o A., Muraki A.,
Vamada M.,
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Q89YP1;
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GO; GO:0004556; F:alpha-amylase activity; 1

GO; GO:0005975; P:carbohydrate metabolism;

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006589; Alp amyl cat_sub.

Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-VPI-5482 / ATCC 29148;
STRAIN-VPI-5482 / ATCC 29148;
MEDLINE=2D550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides
"A genomic view of the human-Bacteroides
Science 299:2074-2076(2003).
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Bacteria; Bacteroidetes; Bact
Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                                                                                                                                    NGVYMQYFEWHLPNDGKLMXQIKEDALHLHDIGVTAVWIPPAYKADEQQDEGYATYDLYD
                                                                                                                                                                                                                                                                                                                                                         NGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
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AQFLDAVRSERGNDFYAVGEYWNGDLEALDAYIEAVGHKVNLFDVPLHYNMFQASQEGKD
                       PDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASKSGGA
                                                                                                   WDWEVDTENGNYDYLMYADLDMDHPEVVTELKXWGKWYVNTTNIDGFRLDAVKHIKFSFF
                                                                                                                                                           ERTKALGEPFEIOGWTGYSFHGRKDKHSDFKWHWYHFSGTGFDDAQKRSGVFQIQGEGKA
                                                                                                                                                                                                DRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA 184
                                                                                                                                                                                                                                           LGEFDQKGTIRTKYGTKDELKKMIDELHKYHIAVYLDVVLNHKAGGDFTEKFMVVEVDPK 122
                                                                                                                                                                                                                                                              LGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
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1.9e-82;
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TICR; SP1382; ...
GO; GO:0004556; F:alpha-amylase activity; IE
GO; GO:0005975; P:carbohydrate metabolism; I
GO; GO:0005975; P:carbohydrate metabolism; I
InterPro; IPR006047; Alpha_amyl_cat
InterPro; IPR006589; Alp_amyl_cat sub.
InterPro; IPR006589; Alp_amyl_cat sub.
InterPro; IPR006589; Alp_amyl_cat sub.
InterPro; IPR006589; Alp_amyl_cat sub.
Pfam; PF00128; alpha-amylase; 1.
R Pfam; PF00128; alpha-amylase.
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Amgiuoli S., Dickinson T., Hickey I Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC BAA-334
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Science 293:498-506(2001).
Science 293:498-506(2001).
EMBL; AE007435; AAK75480.1;
PIR; G95160; G95160.
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Bacteria; Firmicutes; Lactobacillales;
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SMART; SM00642; Aamy; 1.
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SEQUENCE 484 AA; 5591
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                                                                              DRTVELGEPFTINGWTSFTFDGRQDTYNGFHWHWYHFTGTDYDAKRSKSGIYLIQGDNKG
                                                                                                                              DRNOEISGTYOTOAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA
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SEQUENCE 4
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Alpha-amylase (EC 3.2.1.1
AMY OR SPR1239.
                                                                                                                       GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on
GO; GO:0016975; P:carbchydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006589; Alp_amyl cat sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PP00128; alpha-amylase; 1.
PRINTS; PR00110; Alpha-amylase; 1.
PRINTS; PR00110; Alpha-Mylase; 1.
SWART; SM00642; Aamy; 1.
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                                                                                                                                                                                                                                                                                                                                          Glass J.I., "Genome of the bacterium Streptococcus J. Bacteriol. 183:5709-5717(2001). EMBL, AE008495, AAL00043.1; -.
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84 AA; 55880 MW; DA511868187A0FFC CRC64;
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Search completed: May 3, 2004, 20:53:14
Job time: 37.5403 secs

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A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by A;Reference number: 139763; MUID:88137952; PMID:2830166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221 R;Chung, H.S.; Friedberg, F. Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase. A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.; Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the A;Reference number: 139756; MUID:82051296; PMID:6170539
A;Accession: 139756
A;Pathway: glycogen/starch degradation
(;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
(;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <NFT>
F;32-514/Product: alpha-amylase #status predicted <MFT>
F;22-514/Product: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 <RE2>
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A; Residues: 1-514 < TAK>
                                                                                                                                                                                                                                                                                   A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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A; Residues: 1-96 < RES >
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A;Molecule type: DNA
A;Residues: 1-162', R', 164-512 < YUU'>
A;Residues: 1-162', R', 164-512 < YUU'>
A;Residues: 1-162', R', 164-512 < YUU'>
A;Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
A;Experimental source: ATCC 27811
A;Experimental source: ATCC 27811
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338', G', 340-348', S', 350-512 < GRA>
A;Cross-references: GB:M3256; NID:g142510; PIDN:AAA22240.1; PID:g142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylas
A;Accession: A91796; MUID:84185455; PMID:6609154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus licheniformis C;Species: Bacillus licheniformis C;Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000 C;Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000 C;Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844 R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S. J. Biochem. 98, 1147-1156, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete nucleotide sequence of a ases deduced from the DNA sequences. A;Reference number: A91997; MUID:86111694; A;Accession: A91997
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A;Cross-references: GB:K01984; NID:g142432; R;Sibakov, M.; Palva, I. Eur. J. Biochem. 145, 567-572, 1984
                                                                 A; Molecule type: DNA
A; Residues: 1-104 <STE>
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Pred. No. 1.5e-178;
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                                             PIDN: AAA22193.1; PID: g142433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding for heat- and pH-stable alpha-amy
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       片
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    DIGEFHORGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDP
                            DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP
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A; Solecule type: DNA
A; Residues: 1-32, 'I' < GORPA
A; Richin, H; Fietzek, P.P.; Lampen, J.O.

I Bacteriol. 149, 372-373, 1982

A; Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparis A; Ritle: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparis A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
A; Residues: 30-37, 'E', 39-41, 'X', 43-47 < KUHP
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A; Molecule type: DNA
A; Residues: 1-3'H', 5-12', P', 14-47', R', 49-61', 'V', 63', D', 65-67', 'VA'
A; Residues: 1-3'H', 5-12', P', 14-47', R', 49-61', 'V', 63', D', 65-67', 'VA'
A; Residues: 1-3'H', 5-12', PNA of ATCC 14580
A; Note: the authors translated the codon CGT for residue 48 as Gly
A; Laoide, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A; Title: Bacillus 1:oheniformis alpha-amylase gene, amyL, is subjective comber: 139773; MUID:89213924; PMID:2540150
A; Accession: 139774
                                                                                                                                                                                                                                                                                                A;Gene: amyL
G;Function:
G;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Bathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; p;1-29/Domain: signal sequence #status predicted <SIG-
F;1-29/Domain: signal sequence #status predicted <MAT>
F;227-360/Domain: alpha-amylase #status experimental <MAT>
F;230,254/Binding site: calcium (Asn, Asp, His) #status experimental
F;260,290,357/Active site: Asp, Glu, Asp #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B. Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39772
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A, Residues: 1-29 <LAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
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                                           1 VNGTLMQYFEWYTYNDGOHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY
                                                                                                                                                                                                      Similarity
LIGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLY
                                                                                                                                                           Conserva
                                                                                                                                                               FIVE
                                                                                                                                                                                                      82.8%
                                                                                                                                                               41;
                                                                                                                                                                                                      Score 2173; DB 1;
Pred. No. 1.6e-146;
                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                        Length 512;
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120

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A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG-
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;34-519/Domain: alpha-amylase #status experimental <MAT>
F;336-359/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g1
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 15,25-31, 1986
Biochem. Biophys. Res. Commun. 15,25-31, 1986
A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705
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A; Residues: 1-518 < TSU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANRNQETSEEYQIKAWIDFRFPGRGNIYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK
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                                                                                                                                                                                                          GYDMRKLLNSTVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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                                                                                                                                            LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA 121
                                                                                                                                                                                        NGTMMQYFEWYLPNDGNHWNRLNSDASNLKSKGITAVWIPPAWKGASQNDVGYGAYDLYD
AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                       NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKI-SRIFKFRGEGK
                                                                                                                      LGEFNOKGTVRTKYGTRSQLQAAVTSLKNNGIQVYGDVVMNHKGGADATEMVRAVEVNPN
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                         69.6%; Score 1826; DB 1; 66.6%; Pred. No. 6.8e-122; tive 63; Mismatches 90;
                                                                                                                                                                                                                                                                                        Length 518;
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A54541

A54541

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothe:
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothe:
N;Alternate names: 1.4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Tatle: Cloning of a chromosomal alpha-amylase gene from
A;Reference number: A54541
A;Accession: A54541
A;Accession: A54541
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                                                 WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFL
                         WDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                              67.4%; Score 1768.5; DB 1; llarity 65.6%; Pred. No. 8.9e-118; Conservative 56; Mismatches 104;
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A;Molecule type: DNA
A;Residues: 1-549 < JOR>
A;Residues: 1-549 < JOR>
A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
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A;Cross-references: GB:X59476
A;Cross-references: GB:X59476
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on t.
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on t.
C;Comment: Alpha-amylase startue predicted 1,4-alpha-D-glucosidic bonds
A;Cartives: GB:X59476
C;Comment: Alpha-amylase; hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Cartives: GB:X59476
C;Comment: Alpha-amylase; hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Cartives: Cartives: Asp. Asp. Hatharamylase core homology
C;Cartives: Asp. Asp. His)
F;139,237,272/Binding site: calcium (Asp. Asp. His) #status predicted
F;268,298,365/Active site: Asp. Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TROWINHYRSATGKOMPAVAEFWKNDLGAIENYLQKTNWNHSVFDVPLHYNLYNASKSGG 338
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                                                                         NRNOETSEEYOIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA 181
                                                                                                                                                                                       LGEFQQXGTVRTXYGTXSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA 121
                                                                                                                                                   LGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
                                         DRNQEISGTYQIQAWTKFDFFGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA
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A28436

A24436

A24436

A24436

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus plasmid pAT5
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Alba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Molecule type: DNA
A;Residues: 1-549 kNAK>
A;Cross-references: GB:M11450
A;Cross-references: GB:M11450
A;Cross-references: GB:M11450
A;Cross-references: GB:M11450
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A;Cross-references
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A;Genome: plasmid
A;Start codon: GTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies
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Best Local S
Matches 314
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135-54/Product: alpha-amylase #status experimental <MAT>
1235-368/Domain: alpha-amylase core homology <AMY>
139,237,272/Binding site: calcium (Asp, Asp, His) #status
1268,298,365/Active site: Asp, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                           Similarity
KSGLAALITDGFGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
                                                                                                                                 LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA 121
                                                                                                                                                                                                          NGTMMOYFEWYLPODGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
                                                                                                                                                                                                                                           NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYGDYYGI----PQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
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                                                                                                                                                                                                                                                                                                            67.0%; Score 1758.5; DB 1; ilarity 65.4%; Pred. No. 4.6e-117; Conservative 57; Mismatches 104;
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A;Start codon: GTG
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Matches 313
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                                            Local Similarity
mes 313; Conserv
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                                               Conservative
                                          66.9%; Score 1754.5; DB 1; 65.2%; Pred. No. 8.7e-117; tive 58; Mismatches 104;
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A; Molecule type: DNA
A; Mesidues: 1-549 <GRA
A; Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1;
A; Experimental source: genomic DNA of strain NZ-3
A; Experimental source: genomic DNA of strain NZ-3
A; Experimental source: Genomic DNA of strain NZ-3
A; Experimental source: Genomic DNA of strain NZ-3
A; Experimental source: Genomic DNA of Strain NZ-3
A; Pacteriol. 170, 1034-1040, 1988
A; Title: Evidence for movement of the alpha-amylase gene into A; Reference number: I39501; MUID:88139156; PMID:3257753
A; Accession: I39501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3) N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus stearothermophilus C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999 C;Accession: A24549; I39501; I39770 R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986 A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothes A;Reference number: A91817; MUID:86195857; PMID:3009417 A;Accession: A24549
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; po F;1-34/Domain: signal sequence #status predicted <SIG>F;55-549/Product: alpha-amylase #status predicted <NAT>F;25-549/Product: alpha-amylase core homology <AMY>F;139-327,272/Binding site: calcium (Asp, Asp, His) #status predicted F;268,298,365/Active site: Asp, Glu, Asp #status predicted F;268,298,365/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Crooss-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A;Experimental source: strain 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 536-549 <RES
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: 139770
A;Status: translated from GB/EMBL/DDBJ
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A;Reference number: A91804; MUID:86059211; PMID:2999073

A;Contents: pBAM101

A;Contents: pBAM101

A;Contents: pBAM101

A;Contents: pBAM101

A;Accession: A91804

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-29,'Q',31-75,'W',77-122 <TSU>
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the comment of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the code of the 
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A; Residues: 1-548 < 1H1>
A; Residues: 1-548 < 1H1>
A; Residues: 1-548 < 1H1>
A; Cross-references: GB:X02769
A; Cross-references: GB:X02769
A; Experimental source: plasmid pHI300 from strain DY-5
A; Accession: B91999
A; Molecule type: protein
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Residues: 35-48 < 1H2>
A; Takemura, T.; Ihara, H.; Idota, J.
Bacteriol: 164, 1182-1187, 1985
A; Title: Efficient synthesis and secretion of a thermophilic alpha-amylase
A; Reference number: A91804; MUID:86059211; PMID:2999073
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ALBSP
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain I ALBSP alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (). Species: Bacillus stearothermophilus (). Species: Bacillus stearothermophilus (). Species: Bacillus stearothermophilus (). Species: Da-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997 (). Accession: A91999; B91999; A91804; A00845 R; Thara, H.; Sasaki, T.; Tsubol, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S. J. Biochem. 98, 95-103, 1985
J. Biochem. 98, 95-103, 1985
J. Biochem. 98, 95-103, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology A;Reference number: A91999; MUID:86008166; PMID:3876333 A;Accession: A91999
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A;Accession: S15713
A;Molecule type: DNA
A;Residues: 1-493 <MAR>
A;Cross-references: EMBL:X60779; NI
C;Genetics:
A;Gene: amyE
C;Function:
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515713
c) Bacillus circulans
c) Species: Bacillus circulans
c) Species: Bacillus circulans
c) Date: 18-Feb-1994 #sequence_revision 10-Nov-1995
C) Accession: S15713
R; Marcel, T.
                                                                                                                                                                                                                                                                                                                                                A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;200-333/Domain: alpha-amylase core homology <AMY>
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tive 56; Mismatches 111;
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K; lettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heiton, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95160
A;Accession: G95160
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Best Local S
Matches 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGG
                                                                                                                                                                                                                        NRNQETSEEYQIKAWIDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA
                                                                                                                                                                                                                                                                                      LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA 121
                                                                                                                                                                                                                                                                                                                                         NQTLMQYFEWYLPHDGQHWTRLAENAPHLAHLGISHVWMPPAFKATNEKDVGYGVYDLFD
                                                                                                                                                                                                                                                                                                                                                                         NGTIMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
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                                                                                                                                                                                       DRTVELGEPFTINGWISFTFDGRQDTYNGFHWHWYHFTGTDYDAKRSKSGIYLIQGDNKG
                                                                                                                                                                                                                                                                LGEFNOKGTVRTKYGFKEDYLQAIQALKAQGIQPMADVVLNHKAAADHREAFQVIEVDPV 122
GGYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYP
                                                                      FLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQG
                                                                                                           MANEEL VONENGNYDYLMYADLDFKHPEVIQNI YDWADWEMETTGVAGFRLDAVKHIDSF
                                                                                                                                                 WDWE--VSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFS
                                    FMRNF IRDMKEKYGDDFYVFGEFWNPDKEANLDYLEKTEEHFDLVDVRLHQNLFEASOAG
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   46.4%; Score 1217; DB 2; Length 484
47.0%; Pred. No. 1e-78;
tive 81; Mismatches 168; Indels
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P98026

Alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)

Alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)

Alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)

Alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)

Claccession: P98026

R; Delacter 22-Oct-2001 | Streptococcus pneumoniae (strain R6)

R; Hoskins, J.N.; Minkler, M.E.

P; Sun, P.M.; Winkler, M.E.

J; Bacteriol. 183, 5709-5717, 2001

A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A; Reference number: A97872; MUID:21429245; PMID:11544234

A; Residues: 1-484 *KUR>
A; Residues: 1-484 *KUR>
A; Cross-references: GB:AB507317; PIDN:AAL00043.1; PID:g15458876; GSPDB:GN00174

C; Genetics:
A; Gene: amyloridase; hydrolase

C; Keywords: glycosidase; hydrolase
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AKSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEEHVNDGSVSI
                                                                                                                                                                                                                                                                                      WANEEL VONENGNY DYLMY ADLDFKH PEVI ONI Y DWADWFMETTGVAGFRLDAVKHIDSF
                                                                                                                                                                                                                                                                                                                                                               DRTVELGEPFTINGWTSFTFDGRQDTYNGFHWHWYHFTGTDYDAKRSKSGIYLIQGDNKG
                                                          CVFYGDYYGISGQYAQQ--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%; Score 1212; DB 2;
46.6%; Pred. No. 2.4e-78;
ative 84; Mismatches 167;
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CVFYGDYYGISGQYAQE--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN-
                                                                                     QVFYGDMYGTKGTSPKEIPSLKDNIEFILKARKEYAYGPQHDYIDHPDVIGWTREGDSSA
                                                                                                                      ANYDLRGIFTDSLVELKPDKAVTFVDNHDTQRGQALESTVEEWFKPAAYALILLRQDGLP
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R6)

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2 NGTLWQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61 Length 484; Indels 6 Gaps

NQTLMQYFEWYLPHDGQHWTRLAENAPHLAHLGISHVWMPPAFKATNEKDVGYGVYDLFD 62

122 NRNOETSEEYOIKAWIDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA 181 lgefnokgtvrtkygfkedyloaioalkaogiofmadvylnhkaaadhreafovievdfy 122

WDWE--VSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFS 242 239

182

FLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVEDVPLHFNLQAASSQG 299

GGYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYP FMRNFIRDMKEKYGDDFYVFGEFWNSDKEANLDYLEKTEEHFDLVDVRLHQNLFEASQAG 359 302

QVFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSA ANYDLRGIFTDSLVELKPDKAVTFVDNHDTQRGQALESTVEEWFKPAAYALILLRQDGLP 419 419 362

83

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alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
a,Note: Nostoc sp. strain PCC 7120
a,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
c,Pate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
c,Accession: AH2079
R;Kaneko, T:, Nakamura, Y:, Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
NA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A,Tattle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Recession: AH2079
A,Recession: AH2079
B,Catalua: National Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Recession: AH2079
B,Catalua: National Sequence Notational Sequenc
RESULT 12
C86781
alpha-amylase
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A;Cross-references: GB:BA000019; PIDN:BAB73889.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FÖLGEFDQXGSVRTKYGTRQQYLDAVKSLQTHGLQVYADAVLNHKMGGDAVETPKATPFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDDRLNPKGGLQD-----IKTYTHYNFPGRQGKYSNFEWHWWHFDAVDYNEYNSGDRST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHISTWFFPEWIDALERHAGKDLFMVGEYWYNDINTLLWYVDAVRGKMSVFDVPLHYNFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYLLEGKNFDDYVALEKGNFAYLMGCDLDFQNEWVRGEVTYWGKWCLDTTKVDGFRIDAI
                                                                                                                                                                                                                                                                               WNTIGWTRLGDADHPQ-GMAVIMSDGSEGIKWMEVGKPNT--KFIDLTEHIKEAVYTNEW
                                                                                                                                                                                                                                                                                                                                      PDVIGWTREGDSSAAKSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSD
                                                                                                                                                                                                                 GWGEFHVNDGSVSIY 480
                                                                                                                                                                                                                                                                                                                                                                                                        RQEGYPCVFHADYYGAEYEDWGKDGNRYNI FMPSHRWI I DKLLYARKHYAYGPQYNYLDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                            489
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Pred. No. 2.8e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g17131281;
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86791
R;Bolotin, A; Wancker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbackerome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus, Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86781
A;Status: preliminary
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C;Superfamily: alpha-amylase, amyloliquefaciens type;
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A; Residues: 1-491 <STO>
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Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPAN
                                                                                                                                                                                                                                                                                                                 DWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVEDVELHFNLQAASSQGGGY
                                                                                                                                                                                                                                                                                                                                                                                                DWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFLR
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SIY 480
                                        DNKEYGLSCILTNKNGGSKYMIIDKAYAGKVYIDLFGRHEIPITLDQNGGAEFYVNDGSV
                                                                                                                                                          YGDMYGTKGTSPKEIPS-----LKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDS
                                                                                                                                                                                                                          DMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVF 362
                                                                            SAAKSGLAALITDGFGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSV 477
                                                                                                                      WGDLYG-----IPSHNVNPVGDNLRTMIALRKDSEFLRENDYFDHPDIIGWTNILKI 412
                                                                                                                                                                                                                                                                                                                                                              DENVDSENNIFDYLMGADLDFSVSETVEQLEKWGHWFSEMTKIDGFRLDAIKHIDFKYFD
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                                                                                                                                                                                                 DWRTLFDHTLTASQPELSVTFVDNHDTQEGQALQSWIPAWFKEHAYSLILLRKKETPTVF
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Pred. No. 2.6e-72;
5; Mismatches 174;
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alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupor C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002 C;Accession: AD3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Chen et al., RESULT AD3038 A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550; A; Accession: AD3038 ster, E.W. Engineer Agrobacterium tumefaciens PMID:11743193 T.; Levy, R.; Li, Perry, M.; Gordon-Kamm C58. , Woo, I

[imported]

Lactococcus lactis subsp. lactis (strain IL1403)

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A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                       A; Molecule type: DNA
A; Residues: 1-506 < KUR>
                                                                                                                   A; Reference number: A97359; A; Accession: G98247
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                                                           A; Cross-references:
 Map position:
Superfamily:
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Best Local Similarity
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                               Gene: AGR_L
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                                                                                                                                                                                                                                                                                                                                 TNGGSVSVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPAN
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alpha-amylase, amyloliquefaciens type; alpha-amylase
                 linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                           GB:AE007870; PIDN:AAK89505.1;
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43.6%; Pred. No. 7.6e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 183;
                                                         PID:g15159379; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
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kelz, B.;
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                                   VNDGSVSIY
                                                                    IRHGTADA--PGCVVVMSNGEPGEKQADLGPERÅGSVWRDFLGHREEHITLDESGKGTFP
                                                                                                   TREGDSSAAKSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFH
                                                                                                                                                                                                                                            GYDMRRLLDGTVVSRHPEKAVTEVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYP
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A;Reference number: A45738; M
A;Accession: B45738
A;Molecule type: DNA
A;Residues: 1-494 < AMH>
A;Cross-references: GB:L01643
C;Genetics:
                                                                                                                                                                                                                                             A;Gene: amyA
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core ho
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: H18, Glu, Asp #starus predicted
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38.7%; Scc
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vative 77;
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               ed. No. 2.3e-64;
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40 .0%;

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1050;

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2 NGTLMOYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDN-GYGPYDLY

NPTLLQYFHWYYPDGGKLWSELAERADGLNDIGINWVWLPPACKGASGGYSVGYDTYDLF

62 60 Matches

Conservative

471 480	411 422	359 363	299 303	239 243	179 183	121	61
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Search completed: May 3, 2004, 20:54:06 Job time: 15:6493 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
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1 VNGTIMQYFEWYTPNDGQHW......KIGSDGWGEFHVNDGSVSIY 480
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Copyright (c) 1993 - 2004 Compugen Ltd.
          DB
      AMY BACAM
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AMY BACSI

AMY EGOLI

AMY2 ECOLI

AMY3 ORYSA

AMY3 HORVU

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CDGT BACSI

CDGT BACSI

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alpha-amylase: comparison with Baci
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01-JAN-1988 (Rel. 06, Last sequence v
01-JAN-1988 (Rel. 06, Last sequence v
15-MAR-2004 (Rel. 43, Last annotation
Alpha-amylase precursor (EC 3.2.1.1)
glucanohydrolase) (BLA).
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Bacillus licheniformis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                MEDLINE-89213924; PubMed=2540150;
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Shahhoseini M., Ziaei A.A
"An unusual DNA sequence
Submitted (OCT-2001) to t
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A Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
A Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
A Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
T Nucleotide sequence of the maltohexaose-producing amylase gene
T an alkalophilic Bacillus sp. #707 and structural similarity to
T liquefying type alpha-amylases.";
Biochem. Biophys. Res. Commun. 151:25-31(1988).
C -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic lin
C -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic lin
C c in amylaceous polysaccharides so as to remove successive
maltohexaose residues from the non-reducing chain ends.
C -!- COFACTOR; Binds 2 calcium ions and 1 sodium ion per subunit
C similarity).
C -!- PATHWAY: Starch degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98)
Glucan 1,4-alpha-maltohexaosidase) (Exo-maltohexaohydrolase)
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus sp. (strain 707).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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21; Conservative
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM 1 (BY SIMILARITY).
CALCIUM 2 NAD SODIUM (BY SIMILARITY)
CALCIUM 2 NAD SODIUM (BY SIMILARITY)
CALCIUM 1 AND SODIUM (BY SIMILARITY)
CALCIUM 1 AND SODIUM (BY SIMILARITY)
CALCIUM 1 AND SODIUM (BY SIMILARITY)
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1826; DB 1;
; Pred. No. 5.5e-122;
63; Mismatches 90;
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SIMILARITY.

SIMILARITY.

SIMILARITY.

LCIUM 1 (BY SIMILARITY).

LCIUM 2 AND SODIUM (BY SIMILARITY)

LCIUM 2 AND SODIUM (BY SIMILARITY)

LCIUM 2 (VIA CARBONYL OXYGEN) (BY
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EMBL; M18862;

gene."; J. Bact: [2]

Bacteriol. 163:401-406(1985)

Bacillus stearothermophilus. Bacteria; Firmicutes; Bacillales; NCBI\_TaxID=1422; [1]

SEQUENCE FROM N.A. STRAIN=DY5/PHI300; MEDLINE=86008166;

Α., AND

SEQUENCE FROM N.A. STRAIN=NZ-3;

98:95-103(1985).

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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

Surd D, Fujimoto Z, Takase K., Matsumura M., Mizuno H.;

"Crystal structure of Bacillus stearothermophilus alpha-amylase:
possible factors determining the thermostability.";

J. Biochem. 129:461-468 (2001).

I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

IIIKages in oligosaccharides and polysaccharides.

I- COPACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

I- SUBUNIT: Monomer.

I- SUBUNIT: SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P., "Thermostable alpha amylase of Bacillus stearcthermophilus: cloning, expression, and secretion by Escherichia coli."; (In) Chaloupka J., Krumphanzl V. (eds.); Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New York (1007)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86008166; PubMed=3876333; Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Udaka S.; "Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology between prokaryotic and eukaryotic alpha-amylases at the active sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=86059211; PubMed=2999073;
Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
Idota Y., Yamagata H., Udaka S.;
"Efficient synthesis and secretion of a thermophilic alpha-amylase
protein-producing Bacillus brevis 47 carrying the Bacillus
stearothermophilus amylase gene.";
J. Bacteriol. 164:1182-1187(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86195857; PubMed=3009417;
Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Requadt C.;
"Structural genes encoding the thermophilic alpha-amylases c Bacillus stearothermophilus and Bacillus licheniformis.";
J. Bacteriol. 166:635-643(1986).
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EMBL; M57457; AAA22221.1; -.
EMBL; M57457; AAA22221.1; -.
EMBL; M57457; AAA22241.1; -.
EMBL; M57255; AAA22241.1; -.
EMBL; M5725; IPRO06189; Alp amyl cat sub.
InterPro; IPRO06189; Alp amyl cat.
InterPro; IPRO06046; Glyco hydrolase; Glycondry, SMART; SMO0642; AAmy 1.
EMART; SMO0642; AAmy 1.
CAADONATATE metabolism; Hydrolase; Glycondry
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SIGNAL 1 34
CHAIN 3 549
ACT_SITE 268 268
ACT_SITE 272 272
ACT_SITE 365 365
METAL 218 239
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CALCIUM 2 (VIA CARBONYL OXYGEN).

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SODIUM (VIA CARBONYL OXYGEN).

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CALCIUM 3.

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M11450

SEQUENCE FROM N.A.
Suominen I., Karp M.,
"Thermostable alpha a

SEQUENCE OF 1-122 FROM N.A.,

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RESULT S
ANY2 SALTY STANDARD; PRT; 494 P
TO ANY2 STEEL-2003 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update
DT 10-OCT-2003 (Rel. 42, Last annotation update
DT 10-OCT-2003 (Rel. 42, Last annotation update
DT 10-OCT-2003 (Rel. 42, Last annotation update
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RX MEDLINE-9301571; PubMed=1400215;
RX MEDLINE-931534948; PubMed=11677609;
RX MEDLINE-91534948; PubMed=11677609;
RX MEDLINE-12534948; PubMed=11677609;
RX MEDLINE-12534948; PubMed=11677609;
RX MATCHINE, L., Porwollik S., Ali J., Dante N., RA
RYAN E., Sun H., Florea L., Miller W., Storea                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                      large non-coding region.";
J. Gen. Microbiol. 139:1401-1407(1993).
-:- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-:- COPACTOR: Binds 1 calcium ion per subunit (By similarity).
-:- SUBUNIT: Monomer (By similarity).
-:- SUBUNIT: Monomer (By similarity).
-:- SUBCILIULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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STRAINSJW1103;
MEDLINE=93015717; PubMed=1400215;
Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
"Escherichia coli produces a cytoplasmic alpha-amylase, Am
"Escheriol. 174:6644-6652(1992).
J. Bacteriol. 174:6644-6652(1992).
                                                                                                                             SEQUENCE OF 476-494 FROM N.A.
MEDILINE=93381452; Puby#d=8371104;
Raha M., Kihara M., Kawagishi I., Macnab R.M.;
"Organization of the Escherichia coli and Salmonella chromosomes between flagellar regions IIIa and IIIb,
                                                                                                                                                                                                                             MEDLINE=92407478; PubMed=1527488; Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Kawagishi I., Mueller V. williams A.W., Irikura V.M., "Subdivision of flagellar region III of the Escherichi Salmonella typhimurium chromosomes and identification additional flagellar genes.", J., Gen. Microbiol. 138:1051-1065(1992).
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InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SMAKT; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase; G.
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Pred. No. 2e-64;
6; Mismatches 198;
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                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Glycosidase; Calcium-binding;
                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMILARITY).
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Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92407478; PubMed=1527488; Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.; "Subdivision of flagellar region III of the Escherichia coli and Salmqnella typhimurium chromosomes and identification of two additional flagellar genes."; J. Gen. Microbiol. 138:1051-1065(1992).
                                                                                                                                                                                                                                                                                                                                                                 large non-coding region.";
J. Gen. Microbiol. 139:1401-1407(1993).
-:- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic-linkages in oligosaccharides and polysaccharides.
-:- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
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Raha M., Kihara M., Kawagishi I., Macnab R.M.;
"Ozganization of the Escherichia coli and Salmu
chromosomes between flagellar regions IIIa and
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scherichia coli produces a cytoplasmic
Bacteriol. 174:6644-6652(1992).
ween the Swiss Institute . Ther
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'' non-profit institutions as long a
'' non-profit institutions as long a
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license@isb-sib.ch)
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Pred. No. 2.3e-63;
9; Mismatches 195;
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RESULT 7
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ID AM3A\_ORYSA

STANDARD;

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Query Match
Best Local S
Matches 128
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Carbohydr
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SIGNAL
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ACT_SITE
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                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04063; 1AVA. Gramene; P27932; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X56336; CAA39776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
"Characterization of an alpha-amylase multigene cluster in rice.
Plant Mol. Biol. 16:579-591 (1991).
-i- FUNCTION: Important for breakdown of endosperm starch during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. Japonica M202; TISSUE-Etiolated
MEDLINE-91329692; PubMede1714318;
Sutliff T.D., Huang N., Litts J.C., Rodrigu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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AMY1.2 OR AMY3A.
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01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alpha-amylase isozne 3A precursor (EC 3.2.1.1)
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01-AUG-1992
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InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          germination.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COPACTOR: Binds 3 calcium ions per subunit (By similarity).

SUBUNIT: Monomer.

TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.

DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.

SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                           S14958; S14958.
    128;
                  Similarity
                                                                                                                                                                                                                                                                                     Multigene family.
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rate metabolism; Hydrolase; Glycosidase; Calcium-binding;
                                                     176
440
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207
1119
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166
    Conservative
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                13.2%;
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CALCIUM 1 (VIA CARBONYL OX).
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CALCIUM 1 (VIA CARBONYL OX).
Pred. No. 2.96
3; Mismatches
                 Score 346;
Pred. No. 2
                                                                     SIMILARITY)
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                                                                                                 CARBONYL OXYGEN)
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                           Length
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                                                                     SIMILARITY)
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MBL outstation -
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RESULT 8
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DT 10-OCT
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DE Glucan
DE Glucan
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P17859;
01-AUG-1990
01-AUG-1990
10-CCT-2003
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01-AUG-1990 (Rel. 15, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
                                                                                                                                                                                                MEDLINE=90332425; PubMed=2377468;
Yamauchi D., Minamikawa T.;
"Nucleotide sequence of cDNA for alpha-amylase
germinating Vigna mungo seeds.";
Nucleic Acids Res. 18:4250-4250(1990).
                                                                                                                                                                                                                                                                                                                                          Vigna mungo (Rice bean) (Black gram).
Bukaryota; Viridiplante, Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eveurosids I; Fabales; Fabaceae; Papilionoideae; Phasec
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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eudicots; rosid
seoleae; Vigna.
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SEQUENCE FROM N.A.

MEDINE-94120017; PubMed-8290640;

Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;

Tukeuchi H., Yamauchi D., Wada S., Minamikawa T.;

"Nucleotide sequence of the alpha-amylase gene from Vigna mungo

"lant Physiol. 103:1459-1459 [1993].

-i- CANTALYTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic

linkages in oligosaccharides and polysaccharides.

-i- COPACTOR: Binds 3 calcium ions per subunit (By similarity).

-i- SUBUNIT: Monomer (By similarity).

-i- SIBUNATIY: Belongs to family 13 of glycosyl hydrolases.

T.; e from Vigna mungo.

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Matches 121
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EMBL; X73301; CAA51734.1; -.
EMBL; S10514; S10514
HSSP; P04063; 1AVA.
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InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco hydro 13.
Pfam; PF00128; alpha-amylase; 1.
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SM00642; Aamy; 1.
ydrate metabolism;
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                   YGPQHDYIDHPDVIGWTREGDSSAAKSGLAALITDGP
                                     FTTKGILQAA-VQG---ELWRLIDPNGKPPGMIGVKPENAVTFIDNHDT--
                                                                                          VPLHFNIQAASSQGGGYDMRRLLDGT------VVSRHPEKAVTFVENHDTQPGQSLESTVQ
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RNGINEKSTVKIMASEGDLYVAKIDNKIMVKIGP
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46888 MW;
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                                                                                                                    KPDFAVGEKWDSISYGQDGKPNYNQDSHRGALVNWVESAGGAITAFD
                                                                                                                                                                              YLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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15CAODABA3DB4656
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01-AUG-1992
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
MEDLINE=91329692; PubMed=1714318;
Sutliff T.D., Huang N., Lita J.C., Rodriguez R.L.;
"Characterization of an alpha-amylase multigene cluster in plant Mol. Biol. 16:579-591(1991).

-i- FUNCTION: Important for breakdown of endosperm starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2094 (Rel. 43, Last annotation update)
Alpha-amylase isozyme 3C precursor (EC 3.2.1.1)
METAL
SEQUENCE
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-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-9
linkages in oligosaccharides and polysaccharides
-i- COFACTOR: Binds 3 calcium ions per subunit (By s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice)
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                                                                                                                                                                                                                                                                  PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase;
                                                                                                                                                                                                                                                                                                       InterPro; IPR006589; Alp amyl_cat_sub-
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha_amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; X56338; CAA39778.1;
PIR; S14956; S14956.
HSSP; P04063; 1AVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.

TISSUE SPECIFICITY: Germinating seeds.

DEVELOPMENTAL STAGE: Expressed at a high level during ger
in the aleurones cells under the control of the plant hor
in the aleurones cells under the developing grains at a low le
gibberellic acid and in the developing grains at a low le
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CALCIUM 1 (VIA
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CALCIUM 1 AND 3 (B)
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Matches 108;
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Best Local Similarity
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P21543;
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ol-MAY-1991 (Rel. 18, Last sequence update)
ol-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Beta/alpha-amylase precursor [Includes: Beta-amylase (EC 3.2.1.1)].
Alpha-amylase (EC 3.2.1.1)].
Paenibacillus polymyxa (Bacillales; Paenibacillaceae; Paenibacillus polymyxa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAEPO
                SEQUENCE OF 1-776 FROM N.A. STRAIN=ATCC 8523; MEDLINE=87231094; PubMed=2438660;
                                                                                    MEDLINE=89123046; PubMed=2464578; Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H., Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; Tsukagoshi N., Dacterior N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Tsukagoshi N., Yamagata H., Yamaga
                                                                                                                                                                                                               SEQUENCE OF 689-1196 FROM N.A.,
                                                                                                                                                                                                                                             Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H
Tsukagoshi N., Udaka S.;
"Cloning and nucleotide sequence of the gene coding for e
active fragments of the Bacillus polymyxa beta-amylase.";
J., Bacteriol. 169:1564-1570(1987).
                                                                                                                                                                                                                                                                                                                 STRAIN=72;
MEDLINE=87165765; PubMed=2435707;
MEDLINE=87165765; PubMed=2435707;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1406;
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ilarity 24.9%;
Conservative 5
   Strasser J., Friedberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                      N.A
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         InterPro; IPRO06589; Alphamyl_cat_sub.
InterPro; IPRO06040; Alpha amyl_cat.
InterPro; IPRO06040; Alpha amyl_cat.
InterPro; IPRO06047; Alpha amyl_cat.
InterPro; IPRO06046; Glyco_hydro_13.
InterPro; IPRO06046; Glyco_hydro_14.
Pfam; PFO0128; alpha-amylase; 1.
Pfam; PFO0128; alpha-amylase_C; 1.
Pfam; PF001373; Glyco_hydro_14; 1.
Pfam; PF01373; Glyco_hydro_14; 1.
Pfam; PF01373; Glyco_hydro_14; 1.
PRINTS; PRO0110; ALPHAMYLASE.
PRINTS; PRO0150; BETAAMYLASE.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy; 1.
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EMBL; Y00150; CAA68344.1; -.
PIR; A29130; A29130.
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                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00506; BETA AMYLASE 1; 1.

PROSITE; PS00679; BETA AMYLASE 2; 1.

Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
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         degradation;
         BY SIMILARITY.

BY SIMILARITY.

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C-S: 60-FOLD DECREASE IN ACTIVITY.

C-S: 60-FOLD DECREASE IN ACTIVITY.

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N -> S (IN REF. 3).

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N -> KS (IN REF. 3).

NA -> KS (IN REF. 3).

NA -> KS (IN REF. 3).
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BETA-AMYLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91215008; PubMed=1827035;
Uozumi N., Matsuda T., Tsukagoshi N., Udaka S.;
"Structural and functional roles of cysteine residues
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                                                                                                                                                                                                                                                                                                                                                             SECRETION.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages
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D A 48 kDa ALPHA-AMYLASE
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P27937; O1-AUG-1992 (Rel. 23, Created)

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                                                                                                                                                      15-MAR-2004 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alpha-amylase isozyme 3B precursor (EC 3.2.1.1)
glucanohydrolase).
AMY1.6 OR AMY'R
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STRAIN-cv. Japonica M202; TISSUE=Etiolated leaf;
MEDLINE=91329692; PubMed=1714318;
Sutliff T.D., Huang N., Litts J.C., Rodriguez R.
                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                      Oryza sativa (Rice).
                                                                        NCBI_TaxID=4530;
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Pred. No. 4.4e-15;
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 Rodriguez R.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutliff T.D., Huang N., Submitted (MAY-1989) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                linkages in oligosaccharides and polysaccharides. COFACTOR: Binds 3 calcium ions per subunit (By similarity) SUBUNIT: MONDOMET.
TISSUE SPECIFICITY: Germinating seeds.
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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n of an alpha-amylase multigene cluster in rice."; 16:579-591(1991).
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the EMBL/GenBank/DDBJ databases.
for breakdown of endosperm starch
                                                                                                                                                                                                                                                                                                                                                           low level.
                                                                                                                                                                                                                                                                                                                                                                                               germination hormone
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InterPro; IPR006589; Alp\_amyl\_cat\_sub.
InterPro; IPR006047; Alpha\_amyl\_cat.
InterPro; IPR006046; Glyco\_hydro\_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; EMBL; X56337; CAA39777.1; -.
EMBL; M24941; AAA33897.1; -.
PIR; S14957; S14957.
HSSP; P04063; 1AVA.
Gramene; P27937; -. Signal; Multigene family. SIGNAL 1 26 ISOZYME 38

Similarity LMQYFEWYTPNDGQHWKR------LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 174 438 172 169 Conservative AA; 174 172 169 ---ESWKKQGGWYNFLHGHVDDIAATGVTHVWLPP---PSHSVAPQGYMPG 48591 12.2%; X X 54; CALCIUM 1 (BY SIMILARITY)
CALCIUM 1 (VIA CARBONYL C
SIMILARITY).
CALCIUM 3 (VIA CARBONYL C
SIMILARITY).
CALCIUM 1 AND 3 (BY SIMIL ALPHA-AMYLASE I
BY SIMILARITY
BY SIMILARITY
CALCIUM 1 (BY 9 CALCIUM 2 (BY 9 CALCIUM 2 (BY 9 CALCIUM 2 (BY 9 CALCIUM 3 (BY 9 CA Score 319; DB 1; I Pred. No. 2.4e-15; 4; Mismatches 136; B9DE0DB5ABC63F9C 1 (BY SIMILARITY)
1 (VIA CARBONYL C (BY SIMILARITY)
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-ASKYGTGAELRSLIAAFHSKGIKCVADIVINHRC---

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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                         "The alpha-amylase genes in Oryza sativa: characterization clones and mRNA expression during seed germination."; Mol. Gen. Genet. 221:235-244 (1990).

-i- FUNCTION: Important for breakdown of endosperm starch description
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (CLONE POS137).
MEDLINE=9031832; FubMed=2370848;
O'Neill S.D., Kumagai M.H., Majumde
Rodriguez R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Japonica M202; TISSUE=Etiolated MEDLINE=91088278; PubMed=2263460; Huang N. Koizumi N. Redriguez R "Structural organization and differential e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alpha-amylase isozyme 3D precursor (EC 3.2.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                            amylase genes
Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                           DEVELOPMENTAL STAGE: Expressed at a high level during germinal in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                          germination.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COFACTOR: Binds 3 calcium ions per subunit (By similarity)
                                                                                                                                                                            SUBUNIT: Monomer.
TISSUE SPECIFICITY:
                                                                                                                                                                immature seeds. Is the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQN-------NAG
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                                                                                                                                                                                                                                                                                                                                                           Kumagai M.H., Majumdar A., Huang N.,
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                                                                                                                                                             Is expressed in all tissues, except in the most abundant alpha-amylase isozyme
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                                                                                                                                                                                                             subunit (By similarity).
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a; Poales; Poaceae;
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hormone
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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EMBL; M24287;
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SIGNAL 1 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSP; P04063;
                                                                                                                                                                 176
                                                                                                                                         163
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                                                                                                                                                                                                            116 VEVNPANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKF
                                                                                                                                                                                                                                80 RLYDLD-----ASKYGTAAELKSLIAAFHGKGVOCVADVVINHRCAEKKDARGVYCV
                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                          58 DLYDLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAG--ADATEDVTA
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                                                                                                                                                                                                                                                                                                                                          Similarity
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GSTQKLWPFPSDKVMQGYAYILT-HPGVPCIFYDHMF
                                                                                                                                                                 RGEGKAMDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKH
                                                                                                                                                                                                                                                                                                       LMQYFEWYTPNDGQHWKR-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY
                       ESTVOTWEKP----LAYAFILTRESGYPQVFYGDMY 367
                                                                    QSVFDVPLHFNLQAASSQGGGYDMRRLLDGT----VVSRHPEKAVTFVENHDTQPGQSL
                                                                                             YSTDIAKNYVESC----KPGFVVÄEIWNSLSYNGDGKPAANODOGROELVNWVNAVGGP
                                                                                                                   IKFSFLRDWVQAVRQATGKEMFTVAEYWQ----NNAGK----
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73
137
435 AA;
                                                                                                                                                                                                                                                                                                                             Conservative
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AAA33886.1;
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W
                                                                                                                                         ---FGAAPDIDHLNPRVQRELTDWLNWLKSDVGFDGWRLDFAKG
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                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
CALCIUM 3 (VIA CASIMILARITY).
CALCIUM 1 AND 3 (PQ -> R (IN REF.
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Pred. No. 2.8e-15;
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2; Mismatches
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                                               ELWRLRDGNGKAPGMIGWLPEKA
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                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                                                                                                                  Length
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                                                VIFVDNHDI--
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RESULT 13
AM3E\_ORYSA
ID AM3E\_ORYSA

STANDARD;

PRT;

437

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P27934;
01-AUG-1992 (Rel. 23, C
01-AUG-1992 (Rel. 23, L
10-OCT-2003 (Rel. 42, L
Alpha-amylase isozyme 3
glucanohydrolase).
AMY1.4 OR AMY3E.
     METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amylase genes.";
Nucleic Acids Res. 18:7007-7014(1990).
-!- FUNCTION: Important for breakdown of endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=0v. Japonica M202; TISSUE=Etiolated leaf;

MEDLINE=91008278; PubMed=2263460;

Huang N., Kolzumi N., Reinl S., Rodriguez R.L.;

"Structural organization and differential expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59352; AAA33896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JT0946; JT0946.
HSSP; P04063; lAVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Monomer.

TISSUE SPECIFICITY: More abundant in germinating seeds the TISSUE SPECIFICITY: More and callus.

Young leaves and callus.

DEVELOPMENTAL STAGE: Expressed at a high level during ger in the aleurones cells under the control of the plant hor gibberellic acid and in the developing grains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legibberellic acid and in the developing stains at a low legible statement and the statement at a low legible statement at
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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COPACTOR: Binds 3 calcium ions per subunit (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene
173
437
                                                                                                                           168
                                                                             171
       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.
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                                                                                                                           168
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Last sequence update)
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18 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

CALCIUM 1 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

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CALCIUM 3 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 1 (VIA CARBONYL OXYGEN)

SIMILARITY).

CALCIUM 1 (VIA CARBONYL OXYGEN)

SIMILARITY).

CALCIUM 3 (VIA CARBONYL OXYGEN)

SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 1 (VIA CARBONYL OXYGEN)

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CALCIUM 1 (VIA CARBONYL OXYGEN)

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CALCIUM 1 (VIA CARBONYL OXYGEN)

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CALCIUM 1 (VIA CARBONYL OXYGEN)

SIMILARITY).
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419
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                                                                                                                                                                                                                                                                                                                                    118 VNPANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRG
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                                                                                                                                                                                                         GFDGWRLDFAKGYSAPLARIYVDNTNPT----FVVGEIWSSLIYNGDGKPSTNQDADRQ
                                                                                                                                                                                                                                 SLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQ----NNAGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                        LMOYFEWYTPNDGQHWKR-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY
                                                 TLAEIRSRNGIHAESTLDILKAEGDIYVAMIDGKVITKLGPRYDAGGIIPSDFHVVAHGN
                                                                           SL-----KDNIEPILKARKEY-----
                                                                                                                             VENHDTQPGQSLESTVQTWFKP-----LAYAFILTRESGYPQVFYGDMYGTKGTSPKEIP
                                                                                                                                                       ELVNWVEGVGKPATAFDFTTKGILQAA-VQG---ELWRLHDGNGKAPGLMGWMPDQAVTF
                                                                                                                                                                             -LENYLIKTSFNQSVFDVPLHFNLQAASSQGGGYDMRRLLDGT-----VVSRHPEKAVTF
                                                                                                                                                                                                                                                                                  EGKAWDW-----EVSSENGNYD----YLMYADVDYDHPDVVAETKKWGIWYANEL
                                                                                                                                                                                                                                                                                                                                                                                                                  LFOGFNW-----ESWRKQGGWYNFLHEKVEEIASTGATHVWLPP--PSHSVSPQGYMPG
DYCVWEKEG
                        DVIGWTREG
                                                                                                   VDNHDTGSTQSL-----WPFPSDKVMQGYAYILT-HPGIPCIFYDHVF--DWNLQHEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
427
                       415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%;
                                                                                                                                                                                                                                                                                                                                                               -ASKYGTEAELKSLIEAFHDKNVECLADIVINHRC------
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                                                                                                                                                                                                                                                                                                              -----ADYKDSRGVYCVFEGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 315.5;
Pred. No. 4.
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RESULT 14
AMY3_WHEAT
      "A novel wheat alpha-amylase gene (alpha-Amy3).";
Mol. Gen. Genet. 209:33-40(1987).
-i- FUNCTION: Important for breakdown of endosperm
                                                                                                                                    STRAIN=cv. Chinese Spri
Baulcombe D.C., Huttly
                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticem.
                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                 P08117;
01-AUG-1988
                                                                                                                                                                                                                                                                                                                WHEAT
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          glucanohydrolase)
                                                                                                                            Jarvis M.G.;
                                                                                                                                                                            NCBI_TaxID=4565;
                                                                                                                                                                                                                      Triticum aestivum (Wheat).
                                                                                                                                                                                                                                 AMY1.1 OR ALPHA-AMY3
                                                                                                                                                                                                                                                                                                       WHEAT
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                      Spring;
ttly A.K., Martienssen R.A.,
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                                                                                               starch
                                                                                                                                                                                                   Tracheophyta;
aceae; Pooideae;
                                                                                                                                       R.F.,
                          germination hormone
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Query Match
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Matches 110
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SEQUENCE
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EMBL; M16991; AAA34259.1; -.
PIR; S06557; ALWT3
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no ways by non-profit institutions as long as its content is in no ways.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PROOIIC; ALPHI
SMART; SMOO642; Aamy;
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InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
402
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YIDHP----DVIGWTREGDSSAAKSG
                               DKVMQGYAYILT-HPGIPCIFYDHVFDWK-
                                                                                            GVLQEAVQ-
                                                                                                              FNLQAASSQGGGYDMRRLLDGT----VVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKP-
                                                                                                                                                      LDFAKGYSAAMAKIYVD-----NSKPAFVVGELYDRDRQLLANWVRGVGGPATAFDFPTK
                                                                                                                                                                                      IDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLH
                                                                                                                                                                                                                      WGPDEICSDDTKYSNGRGHRDTGGGFDAAPDIDHLNPRVQRELSAWLNWLKTDLGFDGWR
                                                                                                                                                                                                                                                                                                                                              -----NSKYGSGADLKSLIQAFRGKNISCVADIVINHRC-----
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                                                                                                                                                                                                                                                                                                                                                                                                           LFQGFNWESWKTQGGWYKFMQGKVEEIASTGATHVWLPPPSQ--SVSPEGYLPGQLYNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                      LMOYFEWYT-PNDGOHWKRLONDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYDLG
                                                            ----LAYAFILTRESGYPQVFYGDMYGTKGTSPKEIPSLKDNIBPILKARKEYAYGPQHD
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413
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162
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45370
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413
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BY SIMILARITY.
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CALCIUM 2 (BY S
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Pred. No. 4.2e-15;
2; Mismatches 158
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C262ECA1C54FCCE4
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 423
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                                 LKQEITALATVRSRNGI
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CRC64;
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P00633;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanchydrolase) (AMY1) (Low pI alpha-amylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                          SMAKL, Carpo
Germination, Carpo
Calcium-binding,
                                SIGNAL
CHAIN
ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Himalaya;
MEDLINE=83238423; PubM
Rogers J.C., Milliman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006589; Alp amyl_cat_sub
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J01236; AAA32929.1; -. PIR; A00846; ALBH. HSSP; P04063; LAVA.
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SUBCELLULAR LOCATION: Extracellular.

DEVELOPMENTAL STAGE: Production of alpha-amylase is hormonally regulated. Germinating embryos produce the hormone gibberellic acid, which within 10 hours stimulates the aleurone cells covering the endosperm of the seed to produce alpha-amylase. The enzyme then degrades the starch within the endosperm for use by the developing plant embryo.

MISCELLANEOUS: There are at least 4 types of alpha-amylase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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AAW12117	AAB29391	AAB29364	AAW12131	AAB29311	AAB29367	AAE09764	AAW12110	AAE09763	AAE09762	ABU03098	ABU03106	ABU03102	ABU03105	ABU03082	ABG70532	AAP80575	ABU03091	AAG65879	MAIOTOCO
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Alpha-amy	BACILIUS	BACTITUS	Arpna-amy	Bacttrus	BACTTINE	Bacttlus	Alpha-amy	3 Bacttins	Bacttina				Alpha amy				Ampired amy	B. SCEALO	•

## ALIGNMENTS

Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus. 16-OCT-2003 17-JAN-1996 AAR78269; AAR78269 standard; protein; Geobacillus stearothermophilus. Bacillus stearothermophilus alpha amylase (mature protein) 10-AUG-1995 WO9521247-A1 (revised) (first entry) 514 AA

05-OCT-1994; 94WO-DK000371.

02-FEB-1994; 94DK-00000141

(NOVO ) NOVO-NORDISK AS.

Marcher D, Pedersen HH, Nilsson TE;

WPI; 1995-283767/37. N-PSDB; AAQ95033.

Use of an oxidation stable alpha-amylase - for simultaneous desizing bleaching or scouring of fabrics contg. starch or starch derivs.

Claim 8; Page 25; 37pp; English

Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is derived from a Bacillus species. This sequence is the wild type (unmodified) alpha amylase. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 514 AA;

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RRSULT 2
AAR724
ID AAR7
XX AAR7
XX AAR7
XX AAR7
DT 16-C
DT 01-T
XX Baci
XX Baci
XX A1p
XX A1p
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Best Local Similarity
Matches 514; Conserv
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25-MAR-2003
01-DEC-1995
                                                                                                                                                                                                                                                                                                                            Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile thermostable.
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    Borchert TV,
                                                                                   08-OCT-1993;
02-FEB-1994;
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  Bisgard-Frantzen
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94DK-00000140.
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Pred. No. 3.8e-245;
Mismatches 0;
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Best Local S
Matches 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance
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    Bacillus stearothermophilus
                                              17-OCT-2003
11-MAY-1998
                                                                                                                                                         AAW31406
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                                                                                                                                                           standard;
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      Termamy1-like alpha-amylase
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This protein comprises the Termamyl-like alpha-amylase of Bacillus CC stearothermophilus. The invention relates to novel variants of Termamyl-CC like alpha-amylases that have alpha-amylase activity and exhibit an collection in at least one property selected from: substrate specificity; CC binding or cleavage pattern; thermal stability; pH/activity or CC pH/stability profile; stability towards oxidation; Ca2+ dependency and specific activity. The variant has one or more mutations from those CC listed in the specification in relation to Bacillus licheniformis CC Termamyl (see AAW31404). Also claimed are constructs comprising DNA CC conding the variant (see AAV02471-73), and recombinant expression CC vectors and transformed cells containing the DNA. The Termamyl-like alpha CC camylase variant is useful as a detergent additive and can also be used CC in industrial starch processing e.g. liquefaction (claimed) or CC saccharification to produce sweeteners, and in textile desiing CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
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28-JUN-1996;
11-JUL-1996;
08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 515 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Termamyl-like alpha-amylase variants with improved properties - e. increased stability at low pH and low calcium, useful as detergent additives and in industrial starch processing e.g. liquefaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1997.
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                                   FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                                                                                                                                  IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                                   VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                                                                                                                                                                                                        VNPSDRNQEISGTYQ1
                                                                                                            IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
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                                                     The present sequence is a parent alpha-amylase from which mutants with CC increased stability at acidic pH, low calcium concentration and high CC temperatures have been derived. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall chydrophobicity of the enzyme or the overall number of methyl groups in CC the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the CC industrial processing of starch, i.e. starch liquefaction and CC saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid csequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability. Note: According to the specification, the present sequence and the sequence shown in AAY99604 are the same. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Svendsen A,
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                                                                             Andersen C,
Kjaerulff S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Termamy1-like alpha-amylase; variant; starch liquefaction; fuel; detergent composition; laundry cleaning composition; ethanol production; dish washing cleaning composition; hard surface cleaning composition; industrial ethanol production; textile desizing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. stearothermophilus termamyl-like alpha amylase.
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12-FEB-2001
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Best Local Similarity 100.0%;
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                                                                             ABB06935 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGAFDMRTLMTNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
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                                                                          protein; 515 AA
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Pred. No. 3.8e-245;
n: Mismatches 0;
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120

360 300 300 240 240

480

29-AUG-2003 19-JUN-2002

(revised) (first entry)

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Best Local S
Matches 514
                                                                                                                                                                                                                                                                                                                                                                 -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more positions of a group of 31 possible amino acid positions. The alteration in (I) may be at Ang28, Arg181, Asn174, Arg181, Gly182, Asp183, Gly184, Arg186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306, Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444, Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444, Asn445, Lys446, Gln449, Arg454, Asn471, or Asn484. (I) can be used for washing and/or dishwashing, textile desizing, and starch liquefaction. (I) is useful as a component in hard surface cleaning detergent composition, and for producing sweeteners and ethanol from starch. (I) has altered solubility, preferably increased solubility, in particular under washing, dish washing or hard surface cleaning conditions. The present sequence represents a Bacillus stearchermophilus termamyl-like alpha-amylase which is used in the exemplification of the present invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000DK-00000376.
15-MAR-2000; 2000US-0189857P.
23-FEB-2001; 2001UK-00000303.
26-FEB-2001; 2001US-0271382P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1; variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent; washing; sweetener; ethanol; starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel variant of parent termamyl-like alpha-amylase useful as a comin washing and dishwashing compositions, for textile desizing, for liquefaction, and for producing sweeteners and ethanol from starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. stearothermophilus termamyl-like alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                              181
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181
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                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                       DLYDLGEFNOKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                                                                                                      AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALMLPPAYKGTSRSDVGYGVY
                                                                                    VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                                                  DLYDLGEFNOKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                                                                                 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                                                                                                                                                                                                                                                                                      515 AA;
                                                                 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDBSRKLSRIYKFRG
                              IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.8e-245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parent termamyl-like alpha
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The invention relates to a variant of parent TERMAMYI-like alpha-amylase comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339, or at position 234, where the variant has alpha-amylase activity and each position corresponds to a position of a parent Termamyl-like alpha-amylase sequence having a Bacillus lichaniformis alpha-amylase sequence of 483 amino acids, given in specification. The variant alpha-amylase a detergent additive comprising the variant or a detergent composition comprising the variant, is useful for washing and/or dishwashing or textile desizing. The alpha-amylase is useful for starch liquefaction or ethanol production and as a component in a hard surface cleaning the variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic branch linkage cleavage activity of amylopectin or a limit dextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing; starch liquefaction; ethanol production; hard surface cleaner; swe amylopectin; limit dextrin; NOVAMYL; BSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geobacillus stearothermophilus
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09-APR-2002
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                                                                                                                                                                                                                          Claim 5; Fig 1; 84pp;
                                                                                                                                                                                                                                                    New variant of parent Termamyl-like alpha-amylase for use as a component in washing and dishwashing compositions, for textile desizing, for starciliquefaction, and for producing sweeteners and ethanols from starch.
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS20024.
                                                                                                                                                                                                                                                                                                                               WPI; 2002-106123/14.
                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                           A, Jorgensen
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Best Local
14-JUN-2000;
20-JUN-2000;
                                                                                                                                                                                        Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup; starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink; bakery; cereal bar; ice cream; coffee whitener; salad dressing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a natural variant of the TERMAMYL alpha-amylase, BSG. (Updated on 29-AUG-2003 to standardise OS field)
                                               13-JUN-2001; 2001WO-DK000404
                                                                                                                                         Geobacillus stearothermophilus
                                                                              20-DEC-2001,
                                                                                                                                                                                                                                                       Bacillus alpha amylase BSG.
                                                                                                                                                                                                                                                                                                                                                                   AAB47852 standard; protein; 515 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 515 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                       fermented meat; spice.
                                                                                                                                                                                                                                                                                       (first entry)
2000DK-00000917.
2000US-0212852P.
                                                                                                                                                                                                                                                                                                      revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2847; DB 5; 100.0%; Pred. No. 3.8e-245;
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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW

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VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514

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CC (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAB47850-56 show modified alpha-amylases derived from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 32-33; 47pp; English.
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  YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
                                          YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRBGGTBKP
                                                                                                                    SGGAPDMRTIMTNTIMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
                                                                                                                                                                           FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
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                                                                                                                                                                                                                                                                                                       IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
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                                                                                   SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
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Pred. No. 3.
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12-SEP-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to variants of a parent Termamyl-like alpha-amylases. These are used for starch liquefaction, ethanol production, detergent, and textile desizing. The amylases have altered stability, particularly at high temperatures from 70-120plusoC and low pH in the range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-amylase. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variant of parent Termamyl-like alpha amylase, useful in detergent compositions, for starch liquefaction, ethanol production, washing and/or
                                                                                                                                                                                                                                                                                                                                                                  Seguence 515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 5; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thisted T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geobacillus stearothermophilus
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                                                                                                                                                                                                      DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
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                                                                                                                                                 VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                                                                                                                                                                                      AAPFNGTWMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                           FSFFFDWLSYVRSQTGKFLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK 300
                                                                             IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                      VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
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                                                           IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                                                                       Conservative
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; 2000DK-00001354.
; 2000DK-00001687.
; 2001DK-00000655.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                  100.0%; Score 2847; DB 5; 100.0%; Pred. No. 3.8e-245
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21-FEB-2001; 2001US-0270496P.
14-MAY-2001; 2001US-0291122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  starch breakdown catalysis; textile desizing; lignocellulosic tibre; enzymatic de-inking; recycled paper; high-maltose syrup; dough; high glucose syrup; corn-wet milling process; detergent; baking process; beverage; oil field; fuel ethanol; brewing process; staling; starch modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha amylase polypeptide #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 30; Fig 16; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABX08461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified polypeptide with alpha-amylase activity, useful e.g. for iquefying starch, for textile desizing, for treating lignocellulosic lbers, and for producing high-maltose or high-glucose syrup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
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The invention relates to a purified polypeptide with alpha-amylase activity and the polynuclectide encoding it. The polypeptide is useful for hydrolyping starch linkages, for catalysing the breakdown of a starch, for modifying small molecules, for liquefying starch, for washing an object, for textile desizing, for treating lignocellulosic fibers, for improving fibre properties, for enzymatic de-inking of recycled paper pulp, for producing a high-malcose or high-glucose syrup or a mixed syrup, and for increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging fluid formed during production operations and found within the subterranean formation which surrounds a completed well bore. The polypeptide is also useful for preparing a dough or a baked product prepared from the dough and in corn-wet milling processes, detergents,

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                                                                                                                                                                                                          Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction; starch breakdown catalysis; textile desizing; lignocellulosic fibre; enzymatic de-inking; recycled paper; high-malicose syrup; dough; high-glucose syrup; corn-wet milling process; detergent; baking process; beverage; oil field; fuel ethanol; brewing process; staling; starch modification.
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GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW

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420 394

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YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP

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274

180

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120 94

154

YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKP

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The invention relates to a purified polypeptide with alpha-amylase contivity and the polynucleotide encoding it. The polypeptide is useful controlled for hydrolysing starch linkages, for catalysing the breakdown of a construction, for modifying small molecules, for liquefying starch, for washing continuously fibre properties, for treating lignocellulosic fibers, for improving fibre properties, for enzymatic de-inking of recycled paper could, and for increasing the flow of production fluids from a mixed coup, and for increasing the flow of production fluids from a mixed couple for production by removing a viscous, starch-containing, damaging coupleties is also useful for preparions and found within the collegeptide is also useful for preparions and found within the completed from the dough and in corn-wet milling processes, detergents, baking processes, beverages, oil fields (fuel ethanol), brewing processes and starch modification in the paper and pulp industry, for removing considered containing stains from a material and for reducing staling of bakery products. Sequences ABU03040-ABU03144 represent alpha amylase collapse tides of the invention
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Best Local Similarity
Matches 511; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2001; 2001US-0270495P
21-FEB-2001; 2001US-0270496P
14-MAY-2001; 2001US-0291122P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 549 AA;
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                                                                                                                                                                                                                                                                                                                           DLYDLGEFNOKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                        SGGAFDMRTLMTNTLMKDQFTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
                                                                                                                                                                              IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                    VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                              FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                                                                                                                                                                                                          VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                                                                                                                                                                                                                      DLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
                                                                            FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKINGTMSLFDAPLHNKFYTASK
                                                                                                                                                    IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
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Pred. No. 3.9e-243;
1; Mismatches 2;
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25-MAR-2003
12-MAR-1991
                                                                                                                                                                                                                                                      A method is claimed for transforming a host with a recombinant Bacillus alpha-amylase gene, made up of a stearothermophilus N- terminal and a licheniformis C-terminal. The method involves constructing a plaemid with a sequence separating the two terminals containing a unique restriction site which may be cut allowing the plasmid to recombine. See also AAN70539. (Updated on 25-NAR-2003 to correct PA field.) (Updated on 24-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis.
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                                                                                                                                                                                                                                 Sequence 549 AA;
                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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DB; AAN70538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                            VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                           DLYDLGEFNQKGTVRTKYGTKAQYLQA1QAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
                                                                                                                                        AAPPNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                                                                                                           AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
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                 IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                           DLYDLGEFNOKGSVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVE
  IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stearothermophilus
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                                                                                                                                                                           YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP
                                                                                                                                                                                                                                                                                          FSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                             VPRKTTVSTIAWPITTRPWTGEFVRWTEPRLVAW 548
                                                                    VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
                                                                                                    GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                                            GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                                                                          YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKP
                                                                                                                                                                                                               SGGAFDMSTLMNNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW12955
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07-APR-1997
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Geobacillus stearothermophilus.

08-AUG-1996

05-FEB-1996; 96WO-DK000056

03-FEB-1995; 29-MAR-1995; 29-SEP-1995; 06-OCT-1995; 95DK-00000336. 95DK-00001097. 95DK-00001121. 95DK-00000126

(NOVO ) NOVO-NORDISK AS.

Bisgard-Frantzen Ή Svendsen ď Borchert

Alpha-amylase variants - and reduced calcium ion o dependency with improved thermal and oxidation stability

Disclosure; Page 86-88; 111pp; English.

AAW12955, AAW12956, AAR81835 and AAR81836 represent the parent alpha-amylases used to create the variants of the invention (such as AAW12098-W12131). This sequence represents the alpha-amylase from Bacillus stearothermophilus. The variants of the invention were created using site directed, or random, mutagenesis of the INVention were created using site parent alpha-amylases. The variants of the invention can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. The variant alpha-amylases also possess improved specificity to a particular substrate, and/or improved

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specificity with respect to cleavage of substrate. The variants can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in papermaking and beer-making processes. The variants of the invention can also be used in the production of sweeteners and ethanol from starch. (Updated on 16-OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 514 AA;
                                                                                                                                        Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction;
                                                                                                                                                                                                               17-OCT-2003
22-JUL-1999
               30-CCT-1998;
                                           14-MAY-1999
                                                                                                Geobacillus
                                                                                                                            saccharification process.
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                                                                                                                                                                                 stearothermophilus alpha-amylase protein
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               98WO-DK000471
                                                                                                                                                                                                                                                                                 protein;
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Pred. No. 3.7e-239;
2; Mismatches 8;
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Best Local S
Matches 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 514 AA;
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14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                   AAPFNGTMMQYFEWYLFDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         aapengtmqyfeby1tddgtlwtkyanbanlsslgitalwlbaykgtsrsdVgygVy
                                                                                                                                                                   SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILIRQEG
VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW
                                                    GSG1AALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                            YPCVFYGDYYGIFQYNIFSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKF
                                                                                                                                                   SGGTFDMRTLMINTLMKDQPTLAVTFVDNHDTEFGQALQSWVDFWFKFLAVAFILTRQEG
                                                                                                                                                                                                        FSFFPDWLSDVRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK
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                                    GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                          YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKP
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98DK-00000936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.6%;
98.1%;
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Pred. No. 3.7e-239;
2; Mismatches 8;
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standard;

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AAY07383
ID AAY07383
XX
AC AAY07383;
XC AAY07383;
XX Variant;
XW Variant;
XW dishwashir
KW dishwashir
XX Variant appr 13-OCT-19;
XX Variant appr 13-OCT-19;
XX Variant appr 13-OCT-19;
XX (NOVO) NO
XX Yariant appr 13-OCT-19;
XX (NOVO) NO
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                                                                                                                                                                                                                            This sequence represents the parent sequence for new variants of a parent Termanyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variant alpha-amylases - starch liquefaction.
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                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 65-66; 93pp; English.
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                                                                                                                                                                                                            sweeteners or ethanol)
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                                                                                   504;
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514 AA;
                                                                                 97.6%;
llarity 98.1%;
Conservative
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210
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Asn residue"
204
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residue"
214
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residue"
267
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Pred. No. 3.7e-239;
2; Mismatches 8;
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                                           GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                           GSGLAALITDGPGGSKWMYVGKOHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVW
                                                                                                         SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
                                                                                                                                                                                      FSFFPDWLSDVRSQTGKPLFTVGEYMSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK
                                                                                                                                                                                                    FSFFPDMLSYVRSQTGKPLFTVGBYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTASK
                                                                                                                                                                                                                                                    IGKAMDWEVDTENGNYDYLMYADLDMDHPEVTELKNWGKWYVNTTNIDGFRLDAVKHIK 240
                                                                                                                                                                                                                                                                                 VNPSDRNQBISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                           YPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKP
                                                                                                                                         SGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEG
                                                                                                                                                                                                                                    IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTBLKSWGKWYVNTTNIDGFRLDAVKHIK
                   VPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW 514
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Search completed: May Job time : 54.2004 secs ω 2004, 20:50:32

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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Aau07551	Aaw57973	Aaw57981	Aaw57971	Aaw08207	Aau07554	Aaw57978	Aaw57976	Aau07556	Aaw57975	Aau07552	Aaw57979	Abp60489	Abp60490	Abp60491	Abp60495	Abp60492	Abp60494	Abp60493	Aay99771
Bacillus	Alpha-amy	Alpha-amy	Alpha-amy	B.licheni			Alpha-amy		Alpha-amy		-	Bacillus	Bacillus		Bacillus	Bacillus	Bacillus		Bacillus

## ALIGNMENTS

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RESULT 1
AAR78268
ID AAR7
                                                                                                                                                                                 05-OCT-1994;
                                                                                                                                                                                                                                          Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                     AAR78268;
                                                                                                                                                                    02-FEB-1994;
                                                                                                                                                                                                10-AUG-1995.
                                                                                                                                                                                                               W09521247-A1.
                                                                                                                                                                                                                            Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                       Bacillus amyloliquefaciens alpha amylase (mature protein).
                                                                                                                                                                                                                                                                                       17-JAN-1996
                                                                                                                                                                                                                                                                                                                  AAR78268 standard; protein; 480 AA.
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                    94DK-00000141.
                                                                                                                                                                                  94WO-DK000371.
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oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or asp. The parent alpha amylase is derived from a Bacillus species. This sequence is the wild type (unmodified) alpha amylase Claim 7; Page 24; 37pp; English. Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.

N-PSDB; AAQ95032.

1995-283767/37.

Toft AH, Marcher D,

Pedersen HH,

Nilsson TE;

(NOVO ) NOVO-NORDISK AS

Sequence 480 AA;

Query Match

100.0%; Score 2624; DB 2; Length 480;

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RESULT 2
AAW14499
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Matches
                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefacian; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYDMRRLLDGTVVSRHPEKAVTFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANRIQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP
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                                                                                                                                                                                                                                                                                                                                                                 amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                        /label= loop 1 modification region
/note= "preferred region where at least one amino a residue of a parent alpha-amylase (used as a templa a variant) corresponding to this region is deleted replaced with a fragment corresponding to residues of AAW14500; claim 35"
                                                                                                                                                                                                       /label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to this region is deleted or replaced with a fragment
corresponding to residues 13-45 of AAW14500; claim 33"
/label= loop 1 modification region
/note= "at least one amino acid residue of a
-amylase (used as a template for a variant) c
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 480
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                                                                                                                                                                                                                                                                                                                                                                                                          variant.
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deleted or
esidues 14-40
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    03-FEB-1995;
23-OCT-1995;
10-NOV-1995;
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                    Bisgard-Frantzen
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95DK-00001192.
95DK-00001256.
                                                                                                                                                                          96WO-DK000057.
                                                                                                                                                                                                                                                                                    /label= loop 3 modification region /note= "preferred region where at least one amino a residue of a parent alpha-amylase (used as a templa a variant) corresponding to this region is deleted replaced with a fragment corresponding to residues 173 of AAW14500; claim 23"
                                                                                                                                                                                                                                                                                                                                                                                                        196.
                                                                                                                                                                                                                                                                                                                                                                                                                       /label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to this region is deleted or replaced with a fragment
corresponding to residues 165-177 of AAW14500; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195.
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/note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this region is deleted or replaced with a fragment corresponding to residues 102-206 of AAW14500; claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= loop 3 modification region
/note= "at least one amino adid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to this region is deleted or replaced with a fragment
corresponding to residues 98-210 of AAW14500; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "at least one amino acid residue of -amylase (used as a template for a variant) to residues 291-313 of AAW14500 is deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= loop 2 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylases (used as a template fo:
a variant) corresponding to this region is deleted or
replaced with a fragment corresponding to residues 70-78
of AAM/14500; claim 20"
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/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to this region is deleted or replaced with a fragment
corresponding to residues 66-84 of AAW14500; claim 18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= loop 1 modification region
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to residues
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claim 30"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 480 AA;
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Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction;
                                                   Bacillus amyloliquefaciens alpha-amylase protein.
                                                                                      22-JUL-1999
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                                                                                                                                                                                                                                                                                                                                  VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                                                                                                                                                                                                                                                                                                                                                  GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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                                                                                                                                                      protein;
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100.0%; Fred. No. 8.1e-218;
                                                                                      entry)
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    have altered
binding and stability.

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Best Local Similarity
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Kjaerulff S;
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14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Termamyl-like alpha-amylase variants
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                                                                                         GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                                                                                                                                   AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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                                                                                                                                                                                                                  AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                             VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                 LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
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Query Match
Best Local Similarity
Matches 480; Conserv
                                                                                                   amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol)
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-277632/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-1999
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                                                                                                                                                                             This sequence represents the parent sequence for new variants of a parent Termanyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1997;
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                                                                        Sequence
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                                                                          480 AA;
                                                                                                                                                                                                                                                                                             Page 69-70; 93pp;
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hilarity 100.
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                                                                  Variant of parent termamyl-like alpha amylase desizing and starch liquefaction, comprising solvent exposed amino acid residues.
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The present sequence is a parent alpha-amylase from which mutants increased stability at acidic pH, low calcium concentration and hitemperatures have been derived. The sequence encoding this enzyme

Claim 8; Page 59-60; 80pp; English.

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ARESULT 6
AAA7724
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AC AAA7
AC AAA7
XX AAA7
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DT 25-N
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Matches 480
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                                                                                                                                                                                                                          Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile
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01-DEC-1995
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Pred. No. 8.1e-218;
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20-APR-1995

11-MAY-1998 AAW31405; AAW31405

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
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02-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Bacillus derived alpha-amylase variants - having modifications to improve washing and/or dishwashing prodifications
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DB; AAQ88067.
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Pred. No. 8.2e-218;
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Bacillus

amyloliquefaciens

Termamyl-like alpha-amylase

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Matches 480
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28-JUN-1996;
11-JUL-1996;
08-NOV-1996;
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LRDWVQAVRQATGKEMFTVÄEYWQNNAGKLENYLNKTSFNQSVFDVFLHFNLQAASSQGG
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96DX-00000712.
96DX-00000775.
96DX-00001263.
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Pred. No. 8.2e-218;
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sweetener; textile desizing;
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Query Match Best Local Similarity

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Score 2624; DB 4; Pred. No. 8.2e-218;

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Sequence 483

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the parent alpha-amylase

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                                            This sequence represents a termamyl-like alpha amylase. The invention relates to a variant (I) of parent Termamyl-like alpha-amylase comporising alteration at one or more of the positions W13, G48, T49, S50, Q51, A52, D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I) are independently an insertion of an amino acid downstream of the amino acid which occupies the position or deletion or substitution of the amino acid which occupies the position with a different amino acid. The variant in starch liquefaction, in detergent compositions containing it are useful in starch liquefaction, in detergent compositions such as laundry, dish washing and hard surface cleaning compositions, ethanol production such as fuel, drinking and industrial ethanol production, desizing of cleaving, substrate close to the branching point, and further exhibits improved substrate specificity and/or improved specific activity relative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersen C
Kjaerulff
                                                                                                                                                                                                                                                                                                                           New variants of parent Termamyl-like alpha-amylase, useful in starch liquefaction, in detergent compositions and in ethanol production, exhibit altered cleavage pattern relative to the parent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detergent composition; laundry cleaning composition; ethadish washing cleaning composition; hard surface cleaning industrial ethanol production; textile desizing.
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RESULT 9
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XX ABBO
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KW WAXI
KW WASH
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PF 07-P
PR 23-1
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15-MAR-2000; 2000US-0189857F.
23-FEB-2001; 2001UK-0000303.
26-FEB-2001; 2001US-0271382F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1; variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. amyloliquefaciens termamyl-like alpha-amylase
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                       Novel variant of parent termamyl-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.
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RESULT 10
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XX AU12
XX O9-AP
XX Bacil
XX TERMA
KW Starc
KW amylo
XX Sacil
XX Secil

09-APR-2002

entry)

AAU12153

protein;

Bacillus TERMAMYL-like alpha-amylase

BAN.

TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing; starch liquefaction; ethanol production; hard surface cleaner; swe amylopectin; limit dextrin; NOVAMYL; BAN.

sweetener;

Bacillus amyloliquefaciens

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Best Local\S
Matches 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Local\Similarity 100.0%;
nes 480; Conservative 0
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421
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                                                                                                                                                      GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                                                                                                                   LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
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               KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                                                                  GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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 KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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Pred. No. 8.2e-218;
0; Mismatches 0;
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WC200188107-A2

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The invention relates to a variant of parent TERMAMYL-like alpha- amylase comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339, 20 or at position 234, where the variant has alpha-amylase activity and each position corresponds to a position of a parent Termamyl-like alpha- amylase sequence having a Bacillus licheniformis alpha-amylase sequence of 483 amino acids, given in specification. The variant alpha- amylase, a detergent additive comprising the variant or a detergent composition comprising the variant for washing and/or dishwashing or textile desizing. The alpha-amylase is useful for washing to the variant or a detergent composition or cethanol production and as a component in a hard surface cleaning constitute composition, and for producing sweeteners from starch. The variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic branch linkage cleavage activity of amylopectin or a limit dextrin composition (RTM) or NOVANYL (RTM). The present sequence is a component of the TERMAMYL (RTM). The present sequence is a component of the TERMAMYL (RTM).
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Matches 480
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in washing and dishwashing compositions, for textile desizing, for starc
liquefaction, and for producing sweeteners and ethanols from starch.
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KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                              VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                                                                                                                                                  GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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                                                            VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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Query Match Best Local S Matches 480

Similarity

100.0%;

Score 2624; DB 5; Pred. No. 8.2e-218; Mismatches 0;

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VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY

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                                                           The sequences given in AAB47850-56 show modified alpha-amylases derived crome the genus Bacillus. These alpha amylases are Termamyl- like alpha-cromylase and they have been pre-oxidized. The alpha amylase is useful for producing a maltodextrin or glucose syrup, by treating starch with a pre-cxidized alpha-amylase until a product with a DE between 5-45 has been provided and/or until a product with a molecular weight of between 5-30 cc provided and/or until a product with a molecular weight of between 5-30 cc lass been provided. The product comprises a maltodextrin with a DE of 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The cc lapha amylase is useful for producing a maltodextrin or glucose syrup, compared the glucose syrup is useful as an ingredient in food, feed or compared the glucose syrup is useful in confectionery such as creat bars, beverages such as isotomic drinks, bakery such as cereal bars, conditions and ingredients and preparations such as cured consentional foods such as cased the salad dressings, and food ingredients and preparations such as cured meat, fermented meat, spices and seasoning encapsulated flavours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup; starch; food; feed; pharmaceutical; confectionery; candy; isotonic obakery; cereal bar; ice cream; coffee whitener; salad dressing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus alpha amylase BAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified alpha-amylase derived Termamyl-like alpha-amylase, which maltodextrin or glucose syrup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens.
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20-JUN-2000; 2000US-0212852P.
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       Sequence
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12-SEP-2000; 2000DK-00001354
10-NOV-2000; 2000DK-00001687;
26-APR-2001; 2001DK-00000655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Termamyl; alpha amylase; starch liquefaction; textile desizing; detergent; enzyme.
                                                                   This invention relates to variants of a parent Termamyl-like alpha-
amylases. These are used for starch liquefaction, ethanol production,
detergent, and textile desizing. The amylases have altered stability,
particularly at high temperatures from 70-120plusoC and low pH in the
range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
                                                                                                                                                                                                                                                                 Variant of parent compositions, for dish washing, and
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                                                                                                                                                                                                                       Claim 4;
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                                                                                  Washing and cleaning composition, cleaning, contains hybrid amylase
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N-PSDB; ABZ59264.
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Pred. No. 8.2e-218;
; Mismatches 0;
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                                                                                       useful for laundry and har derived from two Bacillus
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Best Local S
Matches 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 483 AA;
                                                                                                                                                                                                                                                                 Key
Peptide
                            08-MAR-1999;
                                                                               16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-amylase; Termamyl-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       amyloliquefaciens Termamyl-like alpha-amylase
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/label= signal
32. .514
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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19-OCT-2000

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 32-34; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-551422/46
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                                                                        VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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                 KSGLAALITDGFGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel thermostable alpha-amylase, useful for improving the preparation of bread, comprises alpha-amylase activity with less than 80% activity after treatment at 65degreesC for 30 min.
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Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Matants
FILL REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-01-30
JEARLIER FILING DATE: 1996-01-10
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JEARLIER FILING DATE: 1996-11-08
JUMBER OF SEG ID NOS: 37
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US-08-194-664A-34
PCT-US94-01553A-34
PCT-US95-10426-34
US-08-600-908A-13
US-09-637-168-2
US-09-636-252A-13
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US-08-468-698-32
US-08-468-698-32
US-08-890-383-3
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CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PAT
ORGANISN: B. amyloliquefaciens
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-09-170-670-5
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APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 100.0%; Score 2624; DB 3; Local Similarity 100.0%; Pred. No. 3.8e-230; les 480; Conservative 0; Mismatches 0;
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Patent Necroation:
Papelicant: Borchert, Torben V.
Papelicant: Svendsen, Allan
Applicant: Nielsen, Carsten
Papelicant: Nielsen, Djarne
Papelicant: Kjaerulff, Soren
Papelicant: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
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GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Struiff, S ren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Carsten
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 5709,000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
CURRENT FILING DATE: 1998-11-16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM, B. amyloliquefaciens
US-09-193-068-5
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Best Local :
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                                                                                                               VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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                       KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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FILE REFERENCE: 5368.200-US
CURRENT FILING DATE: 1998-10-30
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: PA 1998-00936
EARLIER APPLICATION NUMBER: PA 1998-00936
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FBERSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
                                           Sequence 5, Application US/09290734
Patent No. 6361989
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Nielsen, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Sistent Hedegaard
APPLICANT: Nielsen, Helle
TITLE OF INVENTION: No. 6361989el -Amylase And
FILE REFERENCE: 5276.400-US
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; ORGANISM: Bacillus
US-09-183-412-5
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US-09-290-734-5
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Best Local S
Matches 480
              CURRENT APPLICATION NUMBER: US/09/290,734
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; SOFTWARE: FASTSEQ f
; SEQ ID NO 5
; LENGTH: 480
TYPE: PRT
; ORGANISM: B. amylo
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              KSGLAALITDGÐGGSKRYYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                             VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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Pred. No. 3.8e-230;
Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Berchert, Torben
APPLICANT: Berchert, Torben
APPLICANT: Biegard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.304-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR APPLICATION NUMBER: 0712/96
PRIOR APPLICATION NUMBER: 0715/96
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-672-459-4 RESULT 6 US-09-672-459-4 Sequence Patent No. 4. , Application US/09672459 6436888

Query Match Best Local

Similarity

100.0%;

Score 2624; DB 4; Pred. No. 3.8e-230;

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APPLICANT: Duttrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Uibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke And
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT APPLICATION NUMBER: US/09/290,734
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-545-586-5
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US-09-545-586-5
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Patent No. 6528298
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
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                 XSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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APPLICANT: Borchert, Torben
APPLICANT: Bisgard Frantzen, Henrik
APPLICANT: Bisgard Frantzen, Henrik
APPLICANT: Bisgard Frantzen, Henrik
TITLE OF INVENTION: Albha-Amylase Mutants
FILE REFERENCE: 4796.004-US
CURRENT FILING DATE: 2002-06-28
PRIOR PELICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0515/96
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0715/96
PRIOR APPLICATION NUMBER: 0715/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PRILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PRILING DATE: 1996-07-11
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; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4
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Best Local Similarity
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VNGTLMQYFEWYTPNDGOHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY
                                      VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY
                                                                                                                    100.0%; Score 2624; DB 4; ilarity 100.0%; Pred. No: 3.8e-230; Conservative 0; Mismatches 0;
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DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP

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ANRNQETSEEYQIKAWTDFRFFGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP

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APPLICANT: Scendsen, Allan
APPLICANT: Scendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Kjearulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
FILE REFERENCE: 5368.200-US
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
I-ENGTH: 480
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US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
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Best Local
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TYPE: PRT
ORGANISM: Bacillus
-09-769-864-5
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APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Jarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
TITLE OF INVENTION: Polypeptides Having Alkaline Alp
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/291,023A
CURRENT APPLICATION NUMBER: DK 1999 00438
PRIOR APPLICATION NUMBER: DK 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 483
TYPE: PAT
ORGANISM: Bacillus
US-09-291-023A-16
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US-09-291-023A-16
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GENERAL INFORMATION:
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                    KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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100.0%; Pred. No. 3.8e-230;
ative 0; Mismatches 0;
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APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Jorgensen, Christel T.
APPLICANT: Syendsen, Allan
APPLICANT: Syendsen, Allan
APPLICANT: Syendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT FILING DATE: 2000-03-29
EARLIER APPLICATION NUMBER: PA 1999 00437
EARLIER APPLICATION NUMBER: PA 1999 00437
EARLIER APPLICATION NUMBER: 60/127,427
EARLIER FILING DATE: 1999-03-30
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 483
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; Spquence 6, Application Us, Patent No. 6486113; GENERAL INFORMATION: APPLICANT: HATADA, Yuji APPLICANT: IKAWA, Kaori APPLICANT: ITO, Susumu
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US-09-381-687-6
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Best Local Similarity
Matches 480; Conserv
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ORGANISM: Bacillus amyloliquefaciens
-09-537-168-6
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                                                                                                       Application US/09381687
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; TYPE: PRT
; ORGANISM: B. ..
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APPLICANT: OZAKI, Katsuya
TITLE OF INVENTION: MUTDANT ALPHA-AMYLASES
FILE REFERENCE: 2173-0119
CURRENT APPLICATION NUMBER: US/09/381,687
CURRENT FILING DATE: 199-09-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
                                                                                                                                                                Sequence 16, Application US/09540715A
Patent No. 6623948
GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
APPLICANT: Hoeck, Lisbeth
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APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
TITLE OF INVENTION: Enclypeptides Having Alkaline Alj
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILLNG DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR APPLICATION DATE: 201-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
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US-09-540-715A-16
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HAYASHI, Yasuhiro
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Pred. No. 3.8e-230;
; Mismatches 0;
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SEQ ID

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/08/720,899
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US/08/343,804
APPLICATION NUMBER: US/08/343,804
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US-08-720-899-4
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                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bisgaar
APPLICANT: Sorcher
APPLICANT: Svendse
APPLICANT: Theller
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Best Local Similarity
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Patent No.
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TYPE: PRT
ORGANISM: Bacillus
                                                                                                                                                                                                                                      STREET: TO K
CITY: New York
TTATE: New York
                                                                                                                                                                                                                                                                                                                      APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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TH: 483
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5753460
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nilarity 100.0%;
Conservative 0
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Svendsen, Allan
Thellersen, Marianne
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Pred. No. 3.8e-230;
D; Mismatches 0;
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FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPER: amino acids
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                             GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                                                                          <u>LRDWVQAVRQATGKEMPTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG</u>
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KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                  KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                          VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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Pred. No. 4.2e-230;
D; Mismatches 0;
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, sequence 4, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Borchert, Torben Vedel APPLICANT: Svendsen, Allan APPLICANT: Thellersen, Marianne APPLICANT: Van der Zee, Pia TITLE OF INVENTION: AMYLASE VARIANTS NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 5801045
STRRETT. RESULT 15 US-08-459-610-4 COMPUTER READABLE FORM: COUNTRY: CITY: New York 10174-6401 New York E: No. 58010430 No. 5801043disk of No. 5801043th America, 405 Lexington Avenue, 64th Floor USA

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CORREST AFFILCATION DATA:

APPLICATION NUMBER: US/08/459,610
PILING DATE: 02-UN-1995

CILSSIFICATION 1435
PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWINGER: 31,274
REGERENCE/DOCKET NUMBER: 4054.214-US
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION NUMBER: 31,274
REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 4054.214-US
TELEPHONE: 212-867-0123
FILEPAX: 212-867-0123
FILEPAX: 212-867-0123
FILEPAX: 212-867-015
SQUENCE CHARACTERISTICS:
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SQUENCE CHARACTERISTICS:
SQUENCE CHARACTERISTICS:
SQUENCE CHARACTERISTICS:
MOLECULE TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-459-610-4
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Search completed: May 3, 2004, 20:35:56 Job time : 17.2492 secs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                    452
                                                                                                                                                 421 KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
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                                                                                                              KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/2/pubpaa/US06 NEW FUB.pep:*

3: /cgn2=6/ptodata/2/pubpaa/US06 NEW FUB.pep:*

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Gapop 10.0 , Gapext 0.5
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2624
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14
9 US-09-769-864-5

12 US-10-665-667-5

12 US-10-644-187-4

12 US-10-327-837-5

14 US-10-186-042-4

9 US-09-854-346-10

9 US-09-918-543-10

10 US-09-918-543-10

10 US-09-918-543-10

10 US-10-186-376C-10

14 US-10-186-3771-4

14 US-10-184-771-3

14 US-10-184-771-13

14 US-10-184-771-13

14 US-10-081-873-8

14 US-10-081-873-8

14 US-10-081-8733-8
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Sequence 4, Appli
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Sequence 10, Appli
Sequence 10, Appl
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Sequence 10, Appl
Sequence 1, Appli
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US-09-769-864-5
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## ALIGNMENTS

Sequence 5, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:

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APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Nielsen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Niesen, Torben L.
CURRENT FILLOMICANTON: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/99/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
CRAMISM: Bacillus amyloliqufaciens
US-09-769-864-5
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                                                                                                   DIGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP 120
  ANRNOETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK 180
                                                     DIGEFOOKGTVRTKYGTKSELODAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP 120
                                                                                                                                                              VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGFYDLY 60
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Sequence 5, Application US/1066567

Publication No. US20040038368A1

GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Nielsen, Carsten
APPLICANT: Nielsen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: APPLICATION NUMBER: US/10/665,667

CURRENT FILING DATE: 2003-09-19

PRIOR APPLICATION NUMBER: US/09/769,864

PRIOR APPLICATION NUMBER: 09/183,412

PRIOR APPLICATION NUMBER
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Matches 480; Conserv
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LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
                                                                                     AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                                                                                                                                                                                 DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP
                                                                                                                                                    ANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK
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                                                                   AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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241
                                                                                                                                         VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                                                                                                                                                                              GYDWRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 360
                                                                                                                                                                                                                                                               GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 360
                                                                                                                                                                                                                                                                                                                     LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG 300
KSGLAALITDGÞGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                               KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
                                                                                                       VFYGDMYGTXGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0772/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR RILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR RILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO
SEQ ID NO
LENGTH: 480
TYPE: PRI
ORGANISM: Bacillus amyloliquefaciens
US-10-644-187-4 Sequence 4, Application US/10644187 Publication No. US20040048351A1 GENERAL INFORMATION:

ANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK 180 DIGEFQOKGTVRTKYGTKSELODAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP 120 AMDWEVSSENGNYDYLMYADVDYDHYDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF ANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK 180 DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY GYDMRRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTWFKPLAYAFILTRESGYPQ 360 LRDWVQAVRQATGKEMPTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG #WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF GYDMRRLLDGTVVSRHPEKAVTFVENHD? LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG 60 120 240 300 300 240

Indels Length

0

Gaps

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APPLICANT: OLUTTIN, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Ubbeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -Amyl
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/9/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-10-327-837-5
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Publication No. US20030211958A1

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borohert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
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US-10-327-837-5
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                                                                                                                                                       GYDMRRLLDGTVVSRHÞEKAVTFVENHDTQÞGQSLESTVQTWFKÞLAYÁFILIRESGYÞQ
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                  KSGLAAL ITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGBFHVNDGSVSIY
                                                                                     VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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                                                                   VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
                                                                                                                                      GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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RESULT

RESULT 6
US-09-854-346-10
; Sequence 10, Application U;
; Patent No. US20020068352A1
; GENERAL INFORMATION:

US/09854346

480 420 420 360 360 300 300 240

480

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APPLICANT: SPENDEN, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bigard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILLE REFERENCE: 4796.204-US
CURRENT FILLING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR PILLING DATE: 1998-10-29
PRIOR PILLING DATE: 1998-10-29
PRIOR FILLING DATE: 1998-10-29
PRIOR FILLING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 1996-04-30
PRIOR FILLING DATE: 1996-07-11
PRIOR FILLING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILLING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0755/96
PRIOR FILLING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0755/96
PRIOR FILLING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: 0755/96
PRIOR FILLING DATE: 1996-11-08
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Publication No. US20030171236A1
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Best Local Similarity
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TYPE: PRT
ORGANISM: Bacillus
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                            KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                                 VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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APPLICANT: No. US20020068352Alozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REFERENCE: 6140.200-US
CURRENT FILING NOWLER: US/09/854,346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-854-346-10
            APPLICANT: Kjaevulff, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fuglasng, Claus Crone
APPLICANT: Fuglasng, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered pro
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
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US-09-918-543-10
Sequence 10, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574Alozymes
APPLICANT: Thisted, Thomas
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Best Local
ORGANISM: Bacillus amyloliquefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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US-09-925-576C
Sequence 10, Application US/0992576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
ITILE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT APPLICATION DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
SEQ ID NO 10
SEQ ID NO 10
INGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-925-576C-10
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US-09-925-576C-10
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                            Matches 480;
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                                                             DIGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP
                                            VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY
                                                                                                            Conservative
                                                                                                                           100.0%; Score 2624; DB 10; 100.0%; Pred. No. 3.6e-237;
                                                                                                               Mismatches
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Sequence 6, Application US/10146327

publication No. US20030044954A1

GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Syendsen, Allan
APPLICANT: Syendsen, Allan
APPLICANT: Syendsen, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT APPLICATION NUMBER: US/09/537,168
PRIOR APPLICATION NUMBER: DA 199 00437
PRIOR APPLICATION NUMBER: DA 199 00437
PRIOR APPLICATION NUMBER: BA 199-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-03-04

NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
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US-10-146-327-6
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Best Local Simi
Matches 480;
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LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
                                                                                                                                                                           ANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGK 180
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                                                                                      AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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                                                               AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
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100.0%; Pred. No. 3.6e-237;
ative 0; Mismatches 0;
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITITLE OF INVENTION: Alpha-Amylase Mutants
FILLE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
GRGANISM: B. amyloliquefaciens
US-10-184-771-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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    KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGBEHVNDGSVSIY
                                                                                                     VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAA
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RESULT 11 US-10-184-771-13

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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILLE REFERENCE: 0776/17216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
ERIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
FRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 13
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US-10-146-327-2
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Sequence 2, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
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les 449; Conserv
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vo. US20030170769A1
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Pred. No. 3.5e-223; 
, Mismatches 16; Indels 0
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US-10-081-872-114

Sequence 114, Application US/10081872 Publication No. US20030125534A1

GENERAL

INFORMATION:

APPLICANT: Callen, Walter APPLICANT: Richardson, Tob APPLICANT: Frey, Gerhard APPLICANT: Short, Jay M. APPLICANT: Mathur, Eric J.

Toby

APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
APPLICANT: Gray, Kevin A.
APPLICANT: Kerovuo, Janne S.
APPLICANT: Slupska, Malgorzata
ITILE OF INVENTION: ENTWES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
FILE REFERENCE: 09010-108001

CURRENT APPLICATION NUMBER: US/10/081,872

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; TYPE: PRT
; ORGANISM: Bacillus
US-10-146-327-2
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PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                   KSGLAALITDGPGGSKEMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEEHVNDGSVSIY
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NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
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                                                                       VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
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81.7%; Pred. No. 1.9e-196;
tive 37; Mismatches 49;
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 512
TYPER: DET
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Miller, Carl
APPLICANT: Miller, Carl
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Short, Jay
APPLICANT: Short, Jay
APPLICANT: Short, Jay
APPLICANT: Short, Jay
APPLICANT: Mathur, Eric
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-107002
CURRENT APPLICATION UNMBER: US/10/105,733
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 10/081,739
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2001-02-21
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CORGANISM: Environmental
US-10-081-872-114
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US-10-105-733-8
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APPLICANT: Richardson, Tob
APPLICANT: Prey Gerhard
APPLICANT: Miller, Carl
APPLICANT: Kazaoka, Martin
APPLICANT: Short, Jay
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Publication No. US20030138786A1
GENERAL INFORMATION:
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Pred. No. 1.2e-195;
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PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION UNBER: 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEC ID NOS: 69
SOFTWARE: FastSEC for Windows Version 4.
SEC ID NO 8
LENGTH: 512
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Matches 388; Conserv
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NSGLAALITDGPGGAKRMYVGRONAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                                        VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
                                                                       VFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPGHDYIDHPDVIGWTREGDSSAA
                                                                                                              GYDWRKILINGTVVSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
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US-10-081-739A-8
; Sequence 8, Application US/10081739A
; Dablication No. US20030170634A1
; Publication No. US20030170634A1
; GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Miller, Carl
APPLICANT: Miller, Carl
APPLICANT: Martin
APPLICANT: Matchart, Eric
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACT
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE REFERENCE: 09010-10701
; CURRENT APPLICATION NUMBER: 60/270,495
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/29,112
PRIOR APPLICATION NUMBER: 60/290,122
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Unknown
; CHART INFORMATION: Obtained from an environmental sample US-10-081-739A-8
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                                                                                                                                               450 NSGLAALITDGÞGGAKRMÝVGRQNÁGETWHDÍTGNRSEÞVVÍNSEGWGEFHVNGGSVSÍY 509
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                 KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
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Search completed: May 3, 2004, 20:47:46
Job time: 38.3731 secs

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1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/FUUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/backfiles1.pep:*
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  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-09-187-859-2
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US-09-264-097-2
US-09-291-023A-21
US-09-291-023A-21
US-09-537-168-4
US-09-545-586-4
US-09-546-715A-21
US-09-546-715A-21
US-09-769-864-4
US-09-769-864-2
US-08-769-864-2
US-08-683-3804-2
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US-08-683-3804-2
US-08-683-3804-2
US-08-683-3804-2
US-08-683-3804-2
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERNCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1988-10-29
CURRENT FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-06-28
EARLIER APPLICATION NUMBER: 0775/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-2
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US-09-182-859-2
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Patent No. 6143708
GENERAL INFORMATION:
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Best Local (
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LRDWVNHYREKTGKEMPTVABYWONDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG
                                                           AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF
                                                                                      AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF
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100.0%; Pred. No. 2.9e-240;
tive 0; Mismatches 0;
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Sequence 4, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Franta-Amylase Mutants
FILE REFERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER APPLICATION STREET STREET APPLICATION NUMBER: 50/063,306
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Best Local Simi
Matches 483;
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ORGANISM: B. licheniformis
361 VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
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APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, S xen
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REPERANCE: 5709,000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FAILUS DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
GRAANISN: B. licheniformis
US-09-193-068-4
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US-09-193-068-4
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Best Local Similarity
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Pred. No. 2.9e-240;
); Mismatches 0;
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Sequence 4, Application US/09183412

Patent NO. 6204232

GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Nielsen, Djarne
APPLICANT: Nielsen, Djarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Torben L.
APPLICANT: Nielsen, Diarne
JULIANT: Nielsen, Torben L.
APPLICANT: NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: 1240/97
EARLIER APPLICATION NUMBER: 1240/97
EARLIER FILING DATE: 1998-07-11
EARLIER FILING DATE: 1998-07-14
EARLIER FILING DATE: 1998-07-14
EARLIER FILING DATE: 1998-07-14
EARLIER FILING DATE: 1998-07-14
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EARLIER FILING DATE: 1998-07-14
EARLIER FILING DATE: 1998-07-10-08
EARLIER FILING DATE: 1998-07-10-08
EARLIER FILING DATE: 1998-07-10-08
EARLIER FILING DATE: 1998-07-10-08
EARLIER FILING DATE: 1998
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                   VQR 483
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RESULT

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RESULT 6 US-09-291-023A-21

Sequence 21, Application US/09291023A Patent No. 6309871
GENERRAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke

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APPLICANT: No. 6287826man, Barrie Edmund
APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of
TITLE OF INVENTION: From Starch
TITLE OF INVENTION: From Starch
TITLE OF INVENTION: From Starch
TITLE OF INVENTION: From Starch
TITLE OF INVENTION: WIMBER: US/09/264,097
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER APPLICATION NUMBER: 09/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-264-097~2
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Patent No. 6287826
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                               VFYGDMYGTKGDSQRBIPALKHKIBPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
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                          VQR 483
                                                           NSGLAAL:
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Sequence 4, Application US/09290734

Patent No. 6361989

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Bisgard-Frantzen Henrik

APPLICANT: Outcrup, Helle

APPLICANT: Nielsen, Bjarne Ronfeldt

APPLICANT: Nielsen, Vibeke Skovgaard

APPLICANT: Nielsen, Vibeke Skovgaard

APPLICANT: Hoeck, Lisbeth Hedegdard

TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mut

FILE REFERENCE: 5276.400-US

CURRENT APPLICATION NUMBER: US/09/290,734

CURRENT FILING DATE: 1999-04-13
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US-09-290-734-4
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TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 5821.010-US
CURRENT FELLORION NUMBER: US/09/291,023A
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: DX 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus
S-09-291-023A-21
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Best Local Similarity
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Pred. No. 2.9e-240;
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; SOFTWARE: FastSEQ for W.
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B0. lichenifo:
US-09-290-734-4
              Sequence 4, Application US/09537168

Patent NO. 6410295

GENERAL INFORMATION:
GAPPLICANT: Andersen, Carsten
APPLICANT: Andersen, Christel T.
APPLICANT: Hisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/09/537,168
CURRENT APPLICATION NUMBER: PA 1999.0437
EARLIER APPLICATION NUMBER: PA 1999.0437
EARLIER APPLICATION NUMBER: 60/127,427
EARLIER FILING DATE: 1999-03-30
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
TYPE: PRI
ORGANISM: Bacillus licheniformis
TYPE: PRI
ORGANISM: Bacillus licheniformis
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       ORGANISM: Bacillus
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Pred. No. 2.9e-240;
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APPLICANT: SVEINGER, ALLEN, APPLICANT: Biggard-Frantzen, Henrik APPLICANT: Biggard-Frantzen, Henrik TITLE OF INVENTION: Alpha-Amylase Mutants FILE OF INVENTION: Alpha-Amylase Mutants FILE OF INVENTION NUMBER: US/09/672,459; CURRENT APPLICATION NUMBER: 09/182,859; PRIOR APPLICATION NUMBER: 09/182,859; PRIOR FILLING DATE: 1998-00-29; PRIOR FILLING DATE: 1996-04-30; PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-06-28; PRIOR FILLING DATE: 1996-07-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-10; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-10; PRIOR APPLICATION NUMBER: 0705/96; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-10; PRIOR FILLING DATE: 1996-01-10; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-10; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-10; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR FILLING DATE: 1996-01-11; PRIOR APPLICATION NUMBER: 0705/96; PRIOR APPLICATION NUMBER: 0705/96; PRIOR APPLICATION NUMBER: 0705/96; PRIOR APPLICATION NUMBER: 0712/96; PRIOR A
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Best Local Sim:
Matches 483;
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Pred. No. 2.9e-240;
); Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Pjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: NOO-6528298el - Amylase And
ITILE OF INVENTION: NO. 6528298el - Amylase And
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEO ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
IENGTH. 481
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US-09-545-586-4
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 100.0%; Score 2666; DB 4; ilarity 100.0%; Pred. No. 2.9e-240; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 483
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US-09-540-715A-21
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APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Nielsen, Vibeke
APPLICANT: Hoeck, Libbeth
ITILE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 5821.010-US
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PRIOR FILING DATE: 2000-09-28
PRIOR PPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR PPLICATION NUMBER: 0712/96
PRIOR PILING DATE: 1996-06-28
PRIOR PPLICATION NUMBER: 07712/96
PRIOR PILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 2
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US-10-186-042-2
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APPLICANT: Svendsen, Allan
APPLICANT: Berchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10186042
Patent No. 6642044
                                                                                                                                                                                                            Matches 483;
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus
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                                                                            LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                                LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV
                                                                                                                               ANLNGTLMQVFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                                                                                                          100.0%; Score 2666; DB 4; ilarity 100.0%; Pred. No. 2.9e-240; Conservative 0; Mismatches 0;
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APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Niseen, Torben L.
APPLICANT: Kjaerulif, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
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US-09-769-864-4
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Best Local S
Matches 483
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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Bacillus licheniformis
-09-769-864-4
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                                                                          DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK
                                                                                                DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 180
                                                                                                                                               LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                                                                                                                                                                                                    ANLINGTLIMOYFEWYMPNDGOHWRRLONDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                                                                                                                                                                                             100.0%; Score 2666; DB 4; Length 483;
100.0%; Pred. No. 2.9e-240;
tive 0; Mismatches 0; Indels 0
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                                                                ; MOLECULE TYPE: protein US-08-720-899-2
                                                                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH; 512 amino acids
TYPE: amino acid
TYPE: amino acid
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Matches
               Query Match
Best Local Similarity
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APPLICANT: Bisgaa:
APPLICANT: Borche
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-U
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                      TYPE: am:
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Borchert, Torben Vedel
Svendsen, Allan
Thellersen, Marianne
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100.0%; llarity 100.0%; Conservative 0
                                                                                                        linear
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 0
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Score 2666; DB 1;
Pred. No. 3.2e-240;
; Mismatches 0;
                                  Length 512;
   Indels
   0;
 Gaps
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1 ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD 60

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Sequence 2, Application
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard
APPLICANT: Borchert
APPLICANT: Svendser
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US-08-459-610-2
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                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
AFILING DATE: 22-NOV-1994
ATTORNEY/ACENT INFORMATION:
ANDWEY: TO TOWNEY ACENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCE: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America,
STREET: 405 Lexington Avenue, 64th Floor
                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                          NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
ZIP: 10174-6401
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Svendsen, Allan
212-878-9655
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; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-459-610-2
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Best Local Similarity 100.0%; 9
Matches 483; Conservative 0;
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                                                                       450 NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
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                                      481 VQR 483
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VQR 512
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Pred. No. 3.2e-240;
); Mismatches 0;
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Search completed: May 3, 2004, 20:35:55
Job time: 18.3507 secs

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No.
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                Score
                                                  seq length: 0
seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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2666
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Match
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1: /cgn2 6/ptodata/2/pubpaa/US07

2: /cgn2 6/ptodata/2/pubpaa/US06

3: /cgn2 6/ptodata/2/pubpaa/US06

4: /cgn2-6/ptodata/2/pubpaa/US06
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/ Ggn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep: *
/ Ggn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep: *
/ Ggn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep: *
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## ALIGNMENTS

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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Nielsen, Carsten
APPLICANT: Nielsen, Carsten
APPLICANT: Nielsen, Torben L.
APPLICANT: Nissen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
TITLE REFERENCE: 5368.200-US
FILE REFERENCE: 5368.200-US
FILE REPERENCE: 5368.200-US
FILE REPERENCE: 5368.200-US
FILE REPERENCE: 5368.201-01-25
FILE REPERENCE: 5368.201-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILLING DATE: 1998-10-30
NUMBER OF SEG ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
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Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels
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TYPE: PRT
ORGANISM: Bacillus licheniformis
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  121 DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 180
                                                 61 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV
                                                                                  61 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
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Sequence 8, Application US/09854346

Patent No. US20020068352A1

(GENERAL INFORMATION:
APPLICANT: No. US20020068352A1czymes A/S

APPLICANT: No. US20020068352A1czymes A/S

APPLICANT: Svendsen, Allan

APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt

TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity

FILE REFERENCE: 6140.200-US

CURRENT APPLICATION NUMBER: US/09/854,346

CURRENT FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 483

TYPE: PRT

ORGANISM: Bacillus licheniformis
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Matches 483;
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                         LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVFLHYQFHAASTQGG
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   LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG
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Patent No. US20020155574A1

GENERAL INFORMATION:

APPLICANT: No. US20020155574A10zymes A/S

APPLICANT: Thisted, Thomas

APPLICANT: Kjaerulff, Soren

APPLICANT: Kjaerulff, Soren

APPLICANT: Fuglsang, Claus Crone

TITLE OF INVENTION: Alpha-amylase mutants with altered pro;

FILE REFERENCE: 10062.200-US

CURRENT APPLICATION NUMBER: US/09/918,543

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 483

TYPE: PRT

CRGANISM: Bacillus licheniformis
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                                                                                                                             GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                                                                                                             LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG
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NSGLAALITDGPGGAXRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                       VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
                                                                                                             GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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Sequence 30, Application US/09918543
Patent No. US2002015574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A10zymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Adersen, Carsten
APPLICANT: Puglsang, Claus Crone
ITILE OF INVENTION: Alpha-amylase mutants with altered projection of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of th
RESULT 5
US-09-925-576C-8
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; ORGANISM: Bacillus licheniformis
US-09-918-543-30
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  Sequence 4, Application US/1066567
Publication No. US20040038368A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Nielsen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Sienen Sienen
TITLE OF INVENTION: Alpha-Amulase Mutants
TITLE REFERENCE: 5368.200-US
CURRENT APPLICATION UMBERE: US/10/665,667
CURRENT FILING DATE: 2003-09-19
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APPLICANT: Morchert, Torben Vedel
APPLICANT: Molsen, Bjarne Ronfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION UNMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTMARE: Patentin version 3.1
SEQ ID NO
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US-10-665-667-4
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Local Similarity 100.0%; Pred. No. 6.9e-239;
1es 483; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTMARE: FastSEQ for Windows Version 3.
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-665-667-4
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APPLICANT: Svendsen, Allan
APPLICANT: Boschert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796-204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0515/96
PRIOR APPLICATION NUMBER: 0712/96
PRIOR APPLICATION NUMBER: 0775/96
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US-10-644-187-2
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Best Local
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4 LENGTH: 483

CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
RUMBER OF SEQ ID NOS: 35

Amylase Mutants

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PRIOR APPLICATION NUMBER: 1263/96;
PRIOR FILING DATE: 1996-11-08;
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Versic SEQ ID NO 2;
SEQ ID NO 2;
LENGTH: 483;
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-644-187-2
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APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Libbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -A
FILE REFERENCE: 5276.400.US
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                                                                                                                                                   Sequence 4, Application US/10327837 Publication No. US20030211958A1 GENERAL INFORMATION:
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Sequence 4, Application US/10146327

Publication No. US20030044954A1

GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US

FILE REFERENCE: 5886.200-US
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; ORGANISM: B.
US-10-327-837-4
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US-10-146-327-4
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                                                                            CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: PA 199 00437
PRIOR APPLICATION NUMBER: PA 199 00437
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 199-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus
:-10-146-327-4
                                                              SOFTWARE: FastSEQ
SEQ ID NO 4
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Query Match
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Pred. No. 6.9e-239;
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US-10-186-042-2

Sequence 2, Application US/10186042

Publication No. US20030171236A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: BORChert, Torben

APPLICANT: BIGGATG-Frantzen, Henrik

APPLICANT: BIGGATG-Frantzen, Henrik

APPLICANT: BIGGATG-Frantzen, Henrik

APPLICANT: BIGGATG-Frantzen, Henrik

FILE REFERENCE: 4796.204-US

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/10/186,042

CURRENT FILING DATE: 1200-09-28

PRIOR APPLICATION NUMBER: US/09/672,459

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR APPLICATION NUMBER: 0515/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-07-31

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-07-31

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-07-31

PRIOR APPLICATION NUMBER: 0515/96

PRIOR FILING DATE: 1996-07-31

PRIOR APPLICATION NUMBER: 0715/96

PRIOR APPLICATION NUMBER: 0715/96

PRIOR APPLICATION NUMBER: 0715/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION

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APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION UNMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/9/636,252
PRIOR APPLICATION NUMBER: US/9/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO: 2
SEQ ID NO: 2
                                                                                                                                                          ; LENGTH: 512
; TYPE: PRT
; ORGANISM: B.
US-10-184-771-2
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US-10-184-771-2
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                                                                                     Query Match
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Matches 483; Conserv
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Pred. No. 7.5e-239;
Mismatches 0;
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LENGTH: 512 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-199-922-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-199-922-2
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publication No. US20030022346A1
GENERAL INFORMATION:
APPLICANT: Gist-brocades B.V.
TITLE OF INVENTION: Alpha-amylase mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/199,922
FILING DATE: 18-Jul-2002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Wateringseweg 1
CITY: Delft
COUNTRY: The Netherlands
ZIP: 2611 XT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                482;
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                                    1 ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
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ANLNGTIMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
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                                                                                  Conservative
                                                                                                 99.9%;
                                                                                1.
                                                                              Score 2663; DB 14;
Pred. No. 1.4e-238;
1; Mismatches 0;
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                                                                                                                        DB 14;
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480 449 420 389 360 329 300 269

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APPLICANT: KETOVUO, Janne S.
APPLICANT: Slupska, Malgorzata
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR APPLICATION NUMBER: US 60/291,122
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US-10-081-872-114
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SOFTMARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 512
TYPE: PRT
CRGANISM: Environmental
US-10-081-872-114
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Best Local S
Matches 480
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Publication No.
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                                                                                                                              480;
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  61 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                        Similarity
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Frey, Gerhard
Short, Jay M.
Mathur, Eric J.
Gray, Kevin A.
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                                                                                                                              Conservative
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                                                                                                                                     99.5%;
99.4%;
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                                                                                                                            <u>۲</u>
                                                                                                                          Score 2654; DB 14;
Pred. No. 9.8e-238;
2; Mismatches 1;
                                                                                                                              Indels
                                                                                                                                                                  Length 512;
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APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Kazaoka, Martin
APPLICANT: Ric
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-107002
CURRENT APPLICATION NUMBER: US/10/105,733
CURRENT APPLICATION NUMBER: 10/081,739
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 69
SSOTMARE: FastSEQ for Windows Version 4.0
SSOTMARE: FastSEQ for Windows Version 4.0
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                                                                                                          Matches
                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                    LENGTH: 512
TYPE: PRT
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                                               ANLNGTLMQYFEWYMDNDGOHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
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                        ANLNGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                          Conservative
                                                                                                                            99.5%;
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                                                                                                        Score 2654; DB 14;
Pred. No. 9.8e-238;
2; Mismatches 1;
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APPLICANT: KISON, WARTIN
APPLICANT: KAZAOKA, MARTIN
APPLICANT: KAZAOKA, MARTIN
APPLICANT: MACHAY, BYLC
APPLICANT: MACHAY, BYLC
APPLICANT: MACHAY, BYLC
APPLICANT: MACHAY, BYLC
TITLE OF INVENTION: EXZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: EXZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-107001
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/291,122
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 512
TYPE: PRT
ORGANISM: Unknown
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US-10-081-739A-8
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                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-081-739A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                        Query Match 99.5%;
Best Local Similarity 99.4%;
Matches 480; Conservative
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  VFYGDMYGTKGDSQREIPALKHKIEFILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
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                                                                      2;
                                                                            Score 2654; DB 14;
Pred. No. 9.8e-238;
2; Mismatches 1;
                                                                                                                Length 512;
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510 VQR 512		450 NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY 509	421 NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY 480	390 VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 449	361_VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420	330 GYDMRKLLNGTVVSKHPLKAVTTVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 389	301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFIITRESGYPQ 360	270 LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVFLHYQFHAASTQGG 329	241 LRDWVNHVREKTGKEMETVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300	210 AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF 269	181 AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF 240	150 DPADRNRVISGEHRIKAWTHEHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 209	121 DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 180	90 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 149	61 LYDLGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120

Search completed: May 3, 2004, 20:47:45
Job time: 39.6066 secs

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
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2: sp_bacteria:*
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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Q81a84 bacillus ce
Q9rqf4 bacillus me
Q9aq54 bacillus an
Q81yj4 bacillus sp
Q81yj4 bacillus sp
Q81yj4 bacillus sp
Q81yj4 bacillus sp
Q9149 bacillus sp
Q9522 bacillus sp
Q9549 bacillus sp
Q87pf6 vibrio para
Q89yp1 bacillus ci
Q89yp1 bacillus ci
Q89q14 satreptides
Q97q49 streptococc
Q50583 streptococc
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	11.4	11.6	11.6	11.6	12.0		16.8	17.1		17.6	•	•	18.2	•	18.2	38.2	•	•	39.3	•	39.5	40.9			•		44.9	44.9	46.1
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ALIGNMENTS	Q7X9T1	Q8LQK4	Q60224	Q9ZP43	Q94A41	Q9CAR6	Q8JZK3	093647	Q8NKR4	050200	Q8NKR5	033476	Q8U3I9	008452	016460	Q877B1	Q83R40	Q7UAB0	Q8XBB6	Q8FGL8	Q825S5	Q8U916	Q9CG59	068875	Q53786	Q8DT08 .	Q8E0M2	Q8E696	Q8DPC8
TS	Q7x9t1 phaseolus a		natrono	Q9zp43 phaseolus v				ਜ		_			w				0	shigella	escherich	Q8fgl8 escherichia				m	Q53786 streptococc	Q8dt08 streptococc	Q8e0m2 streptococc	Q8e696 streptococc	Q8dpc8 streptococc

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RESULT 1
Query Match
Best Local Similarity
Matches 359; Conser
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01/UUN-2003 (TrEMBLrel. 24, Created)
01/UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630;

MEDLINE=22608415; PubMed=12721630;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattachatyya A., Reznik G., Mikhailova N., Lapidus J.,

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.;

Overbeek R., Kyrpides N.;

"Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q81A$
                                                                  InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; pF00128; alpha-amylase; I.
SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase; Complete proteome.
SEQUENCE 513 AA; 58306 MN; 05C4611C4BFF9FF6 CRC64;
                                                                                                                                                                        Nature 423:87-91(2003).

EMBL; AE017009; AAP10417.1; -.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                         Bacillus anthracis."
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                   76.0%;
74.5%;
   Score 2025; DB 16;
Pred. No. 2.4e-140;
; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
     Indels
                                    Length
                                                                                                                                                                                                                                                                                                                                                               Lapidus A.,
   2;
     Gaps
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NGTLMQYFEWYNDNDGOHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD 63

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RESULT 2
Q9RQT8
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                                                                                                           Matches 356;
                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Jeang C.L., Chen L.S., Chen M.Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067553; AAF00567.1; -
HSSP; P06278; 1VJS.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; F:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006049; Alp amyl cat.
InterPro; IPR006049; Alpha amyl cat.
InterPro; IPR006049; Alpha amyl cat.
InterPro; IPR006049; Alpha amyl cat.
InterPro; IPR006049; Alpha-amylase; 1.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytophaga sp.
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Flexibacteraceae; Cytophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raw starch digesting amylase precursor.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 QQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
   1 ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD 60
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGEFHOKGTVRTKYGTKGELOSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIVV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDWVNHVREKTGKEMFTVABYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRNVEVSGDYEISAWTGFNFPGRGDSYSNFKWKWYHFDGTDWDEGRKLNRIYKFRGIGKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQ--GKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGLATLISDGÞGGAKWMDVGKNNAGEVWYDITGNQTNTVTINKDGWGQFQVSGGSVSIYV 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYGDYYGTKGNSNYEIPALKDKIDPILTARKNFAYGTQRDYFDHPDVIGWTREGDSVHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDWVNHVRQQTGKEMFTVAEYWQNDIQTLNNYLAKVNYNQSVFDAPLHYNFHYASTGNGN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDWEVSSENGNYDYLMYADLDFDHPDVANEMKKWGTWYANELNLDGFRLDAVKHIDHEYL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSFL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGEFNQKGTVRTKYGTKAQLKSAIDALHKKNIDVYGDVVNMHKGGADYTETVTAVEVDPS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVAN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDMRNILKGTVVANHPTLAVTLVENHDSQPGQSLESVVSPWFKPLAYAFILTRAEGYPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDMRKILINGTVVSKHPIKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV 361
                                                                                                                                                                                                                                            58
519 AA;
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                            519 F
58337 MW;
                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                     75.8%;
73.4%;
                                                                                                   60;
                                                                                                       Score 2021; DB 2; Length 519; Pred. No. 4.8e-140; O; Mismatches 67; Indels
                                                                                                                                                                                                                                         POTENTIAL.

RAW STARCH DIGESTING AMYL

; 3E6B88A4DF98B163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                519 AA.
                                                                                                                                                                                                                                                                              AMYLASE
                                                                                                           2
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park K.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:000456; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AQ54 PRELIMINARY; PRT; 533 AA.
Q9AQ54;
Q9AQ54;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSM B-404.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF220440; AAK00598.1; -.
HSSP; F06278; 1VJS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim Y.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus megaterium.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     loning of maltopentaose-producing amylase from Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 IYVQR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 KAKSGLATVITDGPGGSKRMYVGTSNAGEIWYDLTGNRTDKITIGSDGYATFPVNGGSVS 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 PQVFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DPADRNRVISGEHLIKAWTHEHEPGRGSTYSDEKWHWYHEDGTDWDESRKLNRIYKFQ-- 178
64 LGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA 123
                                                                                                                                                                                                                                                358;
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                                                                                                           52 NGTLMQYFEWYAPNDGNEWNRLRTDAENLAQKGITSVWIPPAYKGTTQNDVGYGAYDLYD 111
                                                                                                                                                           4 NGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD 63
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                                                                                                                                                                                                                                                                                                                                                                              533 AA;
                                                                                                                                                                                                                                            Conservative
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AA; 60557 MW; 789CECD6A19C7DDE CRC64;
                                                                                                                                                                                                                                         75.8%; Score 2021; DB 2; 74.3%; Pred. No. 4.9e-140; tive 49; Mismatches 73;
                                                                                                                                                                                                                                                                                                       Length 533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus anthracis (strain Ames). Bacteria; Firmicutes; Bacillales;
                                                                                     GO; GO:0004556; F:alpha-amylase activity; 1
GO; GO:0005975; P:carbohydrate metabolism;
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
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MEDLINE=22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse
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                                                                                                                                                                                                                                                closely related bacteria.";
Nature 423:81-86(2003).
                                                                                                                                                                                                                                                                                                       Thomason B., Fraser C.M.;
                                                                                                                                                                                                           TIGR; BA3551;
                                                                                                                                                                                                                              EMBL; AE017035; AAP27311.1; -.
                                                                                                                                                                                                                                                                                   The genome sequence of Bacillus
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Kolsto A.-B.,
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RESULT 5
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Bacillus sp.
Bacillus sp.
-- ria; Firmicutes;
                                                                                     EMBL; AB008763; BAA32431.1; -.
HSSP; P06278; IVJS.
GO; GO:0004556; F:alpha-amylase activity; I
GO; GO:0004556; P:carbohydrate metabolism;
InterPro; IPR006047; Alpha_amyl cat.
InterPro; IPR006589; Alpha_amyl cat.
InterPro; IPR006589; Alpha_amyl cat.
InterPro; IPR006589; Alpha_amyl cat.
InterPro; IPR006589; Alpha-amylase; 1.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                              MEDLINE=98342096; PubMed=9675143;
Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kob Ozaki K., Ito S.;
"Improved thermostability of a Bacillus alpha-amylase by an arginine-glycine residue is caused by enhanced calcium Biochem. Biophys. Res. Commun. 248:372-377(1998).
EMBL; AB008763; BAA32431.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         082839
                                           SMART; SE
SEQUENCE
                                                InterPro; IPR006046; GIYUU_HY
Pfam; PF00128; alpha-amylase;
PRINTS; PR00110; ALPHAAMYLASE;
SMART; SM00642; Aamy; 1
SMART; SM00642; Aamy; 1
                                                                                                                                                                                                                                                                                                               STRAIN=KSM-1378;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRNVEVSGDYEISAWIGFNFPGRGDNYSNFKWKWYHFDGIDWDEGRKLNRIYKFRGIGKA
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                                                                                                                                                                                                                                                                                                                                 N.A.
                                             Α
                                             58841 MW;
71.6%;
69.1%;
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Score 1909;
Pred. No. 86
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                                               D90A8C90ECC182F8
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9; DB 2;
8e-132;
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Similarity

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Matches
                                                                                                                        STRAIN=ATCC 31195;
da Silva A.C.R., Fernandes E., Pueyo M.T.;
da Silva A.C.R., Fernandes E., Pueyo M.T.;
da Silva A.C.R., Fernandes E., Pueyo M.T.;
Submitted (Nov1997) to the EMBL/GenBank/DDBJ
EMBL, AF032864; AAB86961.1; -
PIR; A54541; A54541
PIR; A54541; A54541
PIR; A54541; A54541
PIR; A54541; A54541
PIR; A54541; A54541
PIR; A54541; A54541
PIR; GO:0004556; F:alpha-amylase activity; IEA
GO; GO:0004556; F:alpha-amylase activity; IEA
GO; GO:0005975; P:carbohydrate metabolism; IE
GO; GO:0005975; P:carbohydrate metabolism; IEA
GO; GO:0005975; P:carbohydrate metabolism; IEA
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GO; GO:0005975; P:carbohydrate metabolism; IEA
GO; GO:0005975; P:carbohydrate metabolism; IEA
GO; GO:0005975; P:carbohydrate metabolism; IEA
GO; GO:0005975; P:carbohydrate metabolism; IEA
GO; GO:000597
               Query Match 67.
Best Local Similarity 64.
Matches 315; Conservative
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O31193;
O1-JAN-1998 (TrEMBLrel. 0)
O1-JAN-1998 (TrEMBLrel. 0)
O1-OCT-2003 (TrEMBLrel. 2)
Alpha amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM
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                                                                                                              62651 MW;
                                        67.1%;
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                    67;
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Last seq
Last ann
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                 Score 1789.5;
Pred. No. 5.2e
57; Mismatches
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                                                                                                                CRC64;
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"Molecular cloning and expression of the gene encoding for "Molecular cloning and expression of the gene encoding for thermostable alpha-amylase of a thermophilic bacterial isc submitted (OCT-1996) to the EMEL/GenBank/DDBJ databases.

EMBL; U75445; AAB18785.1; -.

EMBL; U75445; AAB18785.1; -.

EMGG: 00:0004556; F:alpha-amylase activity; IEA.

RGG; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR006047; Alpha-amyl_cat sub.

R InterPro; IPR006589; Alp_amyl_cat sub.

R InterPro; IPR006046; Glyco_hydro_13.

R InterPro; IPR006046; Glyco_hydro_13.

R Pfam; PF00128; alpha-amylase; 1.
Query Match
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01-FEB-1997 (TrEMBLrel. 0:
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Alpha-amylase precursor.
Bacillus sp. MK 716.
Bacteria; Firmicutes; Bac
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GO; GO:005975; F:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat sub.
InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR0065946; Glyco.hydro_I3.
Pfam; PF00128; Alpha-amylase; 1.
PFANN'S; PR00110; ALPHAMYLASE.
SMARY; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
SGQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CF
                                                                                       Query Match
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Alpha-amylase (RC 3.2.1.1).
Bactillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; Y17557; CAB93517.1; -. PIR; A54541; A54541.
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                                    67;
                              Score 1784.5; DB 2; Length 549; Pred. No. 1.2e-122; 7; Mismatches 99; Indels 5;
                                                                                                                                           8DA3E66DF9120BCE CRC64;
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Query Match
                                                                        InterPro; IFR006047; Alpha_amyl_cat.
InterPro; IFR006589; Alp_amyl_cat_sub.
InterPro; IFR006589; Alp_amyl_cat_sub.
InterPro; IFR006046; GlyCo_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF00186; CBM_20; 1.
Pfam; PF001686; CBM_20; 1.
PFAM; PF00110; ALPHAAMYLASE.
PRINTS; PR00110; ALPHAAMYLASE.
PRODOm; PD001568; CBD_4; 1.
SMARF; SW00642; Aamy 1.
SMARF; SW00642; Aamy 1.
GlyCosidase; Hydrolase.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
Alpha-amylase (EC 3.2.2.1).
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HSSP; P06278; IVUS.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds;
GO; GO:0008477; F:purine nucleosidase activity; IEA.
GO; GO:0008477; F:carbohydrate metabolism; IEA.
                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin L.-L., Chu W.S., Hsu W.H.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=TS-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp. TS-23.
Bactería; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=38441;
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Q93I48;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                 "Isolation of a new Bacillus alpha-amylase."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ d EMBL; ABOS1102; BABF1820.1; -
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha-amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus sp. KSM-K38.
Bacteria; Firmicutes;
NCBI_TaxID=129736;
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L1; Conservative
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8; Mismatches 101;
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Pred. No. 3.2e-118;
2; Mismatches 104;
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C STRAIN=RLMD 2210633 / Serotype 03:K6;

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X Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagom Makino K., Oshima M., Nakano M., Yamashita A., Kubota Y., Kim A Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

A Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mec. of distinct from that of V. cholerae.";

I Lancet 361:743-749(2003).

R EMBL; AP005087; BA662342.1; --

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R Pfam; PF00128; alpha-amylase; 1.
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                                                                     YVQYQVUSTAKAGATMATATASNAAAAAQSAVQTMAAQUAVYWHAYQYMTAAQQQGUUVQYGYY
                                                                                                ANLNGTUMQYFEWYMENDGQHWRRLQNDSAYLAEHGITAVWIFFAYKGTSQA-DVGYGAY
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STRAIN-VPI-5482 / ATCC 29148;
MEDLINE-2250858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides "Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteroidaceae;
NCBI_TaxID=818;
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Bacteria, Bacteroidetes, Bact
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                                                                                                          NGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD
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                                                                                                                                                               Score 1336; DB 16;
Pred. No. 8.9e-90;
4; Mismatches 153;
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GO; GO:0005975; P:carbohydrate metabolism; II
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat. sub.
InterPro; IPR006589; Alp_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat.
InterPro; IPR006046; Glyroo_hydro_I3.
Pfam; PF00128; alpha-amylase; 1.
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                           LGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA
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X Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
A Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kohaza M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
A Yasuda M., Tabata S.,
Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M.,
A Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M.,
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NCBI_TaxID=1313;
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Bacteria; Firmicutes;
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                                                                                                                    GO; GO:0004556; F:alpha-amylase activity; IGO; GO:0005975; P:carbohydrate metabolism; InterPro; IPRO06047; Alpha amyl cat.
InterPro; IPRO06589; Alpamyl cat_sub.
InterPro; IPRO06589; Alpamyl cat_sub.
InterPro; IPRO06589; Alpamyl cat_sub.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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EMBL; AE007435; AAK75480.1;
PIR; G95160; G95160.
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MEDLINE=21357209; PubMed=11463916;
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SM00642; Aamy; 1.
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Query Match

	Search completed: May 3, 2004, 20:53:12 Job time : 38.3365 secs	QOD Seas
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478	420 -QŚPIAVLISNDQENSKSMFVGQEWTNQTFVDLLGNHQGQVTIDEEGYGQFPVSARŚVŚV 478	В
479	420 ANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHYNGGSVSI	Ş
419	363 CVFYGDYYGISGQYAQEDFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN-	뮍
419	360 QVFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSV	Ş
362	303 ANYDLRGIFTDSLVELKPDKAVTFVDNHDTQRGQALESTVEEWFKPAAYALILLRQDGLP	g D
359	300 GGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQBGQSLESTVQTWFKPLAYAFILTRESGYP	Qy
302	243 FMRNFIRDMKEKYGDDFYVFGEFWNPDKEANLDYLEKTEEHFDLVDVRLHQNLFEASQAG	рb
299	240 FLRDWVNHVRBKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQG	8
242	183 WANEELVDNENGNYDYLMYADLDFKHPEVIQNIYDWADWFMETTGVAGFRLDAVKHIDSF	망
239	182 WDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFS	δ
182	123 DRTVELGEPFTINGWTSFTFDGRQDTYNGFHWHWYHFTGTDYDAKRSKSGIYLIQGDNKG	da
181	124 DRNRVISGEHLIKAWTHFHFDGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGKA	Ş
122	LKAQGİQPMADVVLNHKAAADHREAFQVIEVDPV	В
123	64 LGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA 123	Ş
62	3 NQTLMQYFEWYLPHDGQHWTRLAENAPHLAHLGISHVMMPPAFKATNEKDVGYGVYDLFD	В
63	4 NGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD	Ş
4.	Best Local Similarity 48.6%; Prod. No. 3.3e-82; Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps	X 80

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Title:
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P27932 oryza sativ

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P1747 bacillus sci

P27937 oryza sativ

P08137 bacillus ci

Q97789 schizosacch

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MEDLINE=21125602; PubMed=11226887;

Suvd D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;

"Crystal structure of Bacillus stearothermophilus alpha-amylase:
possible factors determining the thermostability.";

J. Biochem. 129:461-468(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunisubuni: Monomer.

SIMULARITY: Belongs to family 13 of glycosyl hydrolases.
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P19571;
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O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)
(Maltohexaose-producing amylase) (Exo-maltohexaohydrolase).
Bacillus sp. (strain 707).
Bacillus sp. (strain 707).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                 Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
"Nucleotide sequence of the maltohexaose-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amylases.";
Biochem. Biophys. Res. Commun. 151:25-31(1988).
-i- CAPALTYTIC ACTIVITY: Hydrolysis of 1.4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltohexaose residues from the non-reducing chain ends.
-i- COPACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE (MEDLINE=88162814; PubMed=3258152;
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1416;
similarity).

PATHWAY: Starch degradation.
SUBCELLULAR LOCATION: Secreted
SIMILARITY: Belongs to family
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InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
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                              LALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVWV
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STRAIN=ATCC 27811;
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MEDLINE=21992788; PubMed=11997021;

Kandra L., Gyemant G., Remenylk J., Hovanszki G., Liptak A.;

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STRAIN-ATCC 6598;
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Declerck N., Joyet P., Gaillardin
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MUTAGENESIS OF TRP-292 AND VAL-315.
STRAIN=ATCC 27811;
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                          X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
H162V/N219F/A238V/Q293S/N294Y.
STRAIN-ATCC 6598,
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"Crystal structure of calcium-depleted amylase at 2.2-A resolution.";
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       IGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIK
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BIOTECHNOLOGY: Used in the food industry f liquefaction of starch-containing mashes a industry to remove starch. Sold under the
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EMBL; M38570; AAA22240.1; -.
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EMBL; AF438149; AA0226743.1; -.
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InterPro; IPR006046; Glyco_hydro_13.
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Pfam; PF00128; alpha-amylase; 1.
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SEQUENCE OF 32-222.
MEDLINE=80241725; PubMed=6156671;
MEDLINE=0241725; PubMed=6156671;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-96 FROM N.A.

MEDLINE=82051296; PubMed=6170539;
Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
Soederlund H., Takkinen K., Kaeaeriaeinen I.;
"Nucleotide sequence of the promoter and NH2-terminal signal peptide
region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
Gene 15:43-51(1981).
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                                       X-RAY CRYSTALLOGRAPHY (1.9 MEDLINE=20384196; PubMed=10 Brzozowski A.M., Lawson D.N
                                                                                                                                     SEQUENCE OF 1-39 FROM N.A.

MEDILINE=88137952; PubMed=2830166;

Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C.,

"Efficient secretion of Bacillus amyloliquefaciens alpha
its own signal peptide from Saccharomyces cerevisiae hos
gene 59:161-170(1987).
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Pfam; PF00128; alpha-amylase; 1.
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J. Gen. Microbiol. 138:1051-1065(1992).
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28-FB2003 (Rel. 41, Last.sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
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SEQUENCE OF 476-494 FROM N.A. MEDILINE=93381452; PubMed=8371104; Raha M., Kihara M., Kawagishi I., Macnab R.M.; "Organization of the Escherichia coli and Salmu chromosomes between flagellar regions IIIa and
                                                                                                                                                                                                                                               SEQUENCE OF 1-6
STRAIN=SJW1103;
                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Leonard S., Sun H., Florea L., Miller W., Stoneking T., Nhan Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 70072
MEDLINE=21534948; PubMed=11677609;
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WEDLINE=93015717; PubMed=1400215;
WEDLINE=93015717; PubMed=1400215;
Raha M., Kawagishi I., Mueller V., Kihara
"Escherichia coli produces a cytoplasmic a
J. Bacteriol. 174:6644-6652(1992).
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  and Salmonella IIIa and IIIb,
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identification of
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alpha-amylase, Am
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  typhimurium including a
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Matches 216
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SEQUENCE
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J. Gen. Microbiol. 139:140
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EMBL; AB008787; AALZ0875.1; -.
EMBL; M85241; AAAZ7079.1; -.
EMBL; L13280; AAAZ71970.1; -.
EMBL; L13280; B45738.
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InterPro; IPR006589; Alp amyl_cat
InterPro; IPR006047; Alpha_amyl_cat
InterPro; IPR006047; Alpha_amyl_cat
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
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CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

COPACTOR: Binds 1 calcium ion per subunit (By similarity).

SUBCUNIT: Monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic.
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                                                              PSVFYPDLYGASYEDSGENGETCRVDMPVI-NQLDRLILARQRFAHGIQTLFFDHPNCIA
                                                                                                       PCVFYGDYYGIP-
                                                                                                                                              GAEYDWRHIFTGTLVEADFFHAVTLVANHDTQPLQALEAFVEFWFKPLAYALILLRENGV
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494 AA;
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56522 MW;
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5C1E862FEDD5E47C CRC64;
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RESULT 6
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01-AUG-1992 (Rel. 23, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                          Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomuri Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Tasito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map DNA Res. 3:379-392(1996).
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                                                                                                                                                                                                                     MEDIINE-92407478; PubMed=1527488;
Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab
"Subdivision of flagellar region III of the Escherichia coli a
Salmonella typhimurium chromosomes and identification of two
additional flagellar genes.";
J. Gen. Microbiol. 138:1051-1065(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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STRAIN=K12 / MG1655;
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Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
"Bscherichia coli produces a cyroplasmic alpha-amylase, AmyA.";
J. Bacteriol. 174:6644-6652(1992).
                                                                                                 MEDLINE=93381452; PubMede=8371104;
Raha M., Kihara M., Kawagishi I., Macnab R.M.;
"Organization of the Escherichia coli and Salmonella typhimurium
"Organization of the Escherichia oli and IIIb, including a
chromosomes between flaggilar regions IIIa and IIIb, including a
                                                                                                                                                                         SEQUENCE OF 475-495 FROM N.A. STRAIN=JA11;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-5 FROM N.A. STRAIN=JA11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMYA OR B1927
large non-coding region.";

J. Gen. Microbiol. 139:1401-1407(1993).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

-!- SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97251358; PubMed=9097040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                on the linkage map.";
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GEGWNDQVDDELGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQTQCDGFRLDAVKHIPA

123 182 183

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302 303 362 363 412

423

SRSGTDEFP--GCVVVMSNGDDGEKTIHLGENYGNKTWRDFLGNRQERVVTDENGEATFF

471

PSVEYPDLYGAHYEDVGGDGQTYPIDMPIIEQLDELILARQRFAHGVQTLFFDHPNCIAF TREGGTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFK

**な 品 な 品 な 品** 

PCVFYGDYYGIPQYNIPS

GRDYDMTQIFTGTLVEADPFHAVTLVANHDTQPLQALEAPVEPWFKPLAYALILLRENGV

-LKSKIDPLLIARRDYAYGTQHDYLDHSDIIGW

411

422

122 181 182 182 241 242 242 301 301

362

GGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGY

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                                                                                                                              CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                       EcoGene; EG11387; amyA.
InterPro; IPR006589; Alp amyl cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
Pfam; PR00128; alpha-amylase; 1.
SMART; SM00642; Amy; 1.
                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000285; AAC74994.1; --
EMBL; D90833; BAA15755.1; --
EMBL; M85240; -; NOT ANNOTATED_CDS.
EMBL; L13279; AAA82575.1; --
PIR; D64956; A45738.
HSSP; P06278; 1VJS.
                                                                                                                                                                                                                                                    ACT_SITE

    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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                                                                                210;
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                                                                                            Similarity
DLGEENQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEMVDAVEVNP
                                           NGTMMQYFEWYLFDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRS-DVGYGVYDLY
                                                                                                                                                                                                                                                                  proteome.
                               NPTLLQCFHWYYPEGGKLWPELAERADGFNDIGINMVWLPPAYKGASGGYSVGYDSYDLF
                                                                                                                                                                                                      235
265
332
239
                                                                                Conservative
                                                                                                                                                                                                                                                                                metabolism;
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149
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56639 1
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265
232
239
                                                                                             42.9%;
                                                                                                        37.7%;
                                                                                                                                                                                                                                                                                Hydrolase; Glycosidase; Calcium-binding;
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                                                                                83;
                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYG
SIMILARITY)

XL -> SS (IN REF. 1).
A -> V (IN REF. 1).
O -> E (IN REF. 1).
O -> E (IN REF. 1).
                                                                                Pred. No. 4.36
3; Mismatches
                                                                                            Score 1074.5; DB Pred. No. 4.3e-69;
                                                                                                                               -> V (IN REF. 1).
-> E (IN REF. 1).
-> I (IN REF. 1).
26AFF6797DDA54D6 CRC64;
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472 VNGGSVSVWV CNGGSVSVWV 490

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RESULT 7
        EMBL; M28053; AAA22310.1; -.
HSSP; P43379; 1CDG;
InterPro; IPR006689; Alp amyl_cat_sub.
InterPro; IPR006648; Alpha_amyl_c.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; CBD 4.
InterPro; IPR006046; GlyGo_bydro_13.
InterPro; IPR006046; GlyGo_bydro_13.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR0072909; IPT TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00128; alpha-amylase_C; 1.
Pfam; PF00686; alpha-amylase_C; 1.
Pfam; PF00686; alpha-amylase_C; 1.
Pfam; PF00686; alpha-amylase_C; 1.
Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.

MEDLINE=90257592; PubMed=2534600;

Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;

"Construction of a chimeric series of Bacillus cyclomalicodextrin glucanotransferases and analysis of the thermal stabilities and I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UUI-1993 (Rel. 26, Created)
01-UUI-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor
(Cyclodextrin-glycosyltransferase) (CGTase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sp. (strain 17-1).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optima of the enzymes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1409;
                                                                                                                                                               PRINTS; PRO0110; ALPHAAMYLASE.
PTCDOm; PD001568; CBD 4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy; 1.
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CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALICOLIGOSACCHARIDE PRODUCED.
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a 1,4-alpha-D-glucosidic bond.
COFACTOR: Binds 2 calcium ions per subunit (By similarity).
SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
                                      166
230
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523
                                                                                                                                                  Glycosyltransferase; Calcium-binding; Signal
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          27
713
165
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          E.
BY SIMILARITY
                                                       C 28.
                                                                                                   CYCLOMALIODEXTRIN GLUCANOTRANSFERASE. A1.
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RESU AMYB AC DT DT DE DE	Db Qy	2	D O D O O	Db Qy MA							
LT 8 PAEPO AMYB PAEP P21543; 01-MAY-19 01-MAY-19 15-MAR-20 Beta/alpha-amy	E E C C	2 8 7 4 2 8 5 8 7 8	181 212 240 262 298 319	tches 133- 19 67 63 127 121	ACT_SITE ACT_SITE ACT_SITE ACT_SITE ACT_SITE ACTAL METAL	S: 1 (Rel 1 (Rel 4 (Rel -amyla	-PITTRP 4  : :  GPMWAKP 5	PLAYAFILTRO	IGKAWDWEVD:	CODSe	284 355 54 56 59 60 70 226 226 227 70 713 P
NDARD; 18, Crea 18, Last 43, Last precurs 3.2.1.1)	98 38	EGYPC       RGVPA QHDYL QHDYL TQERW FYDLT ;   ;	TENGIYI	ਜ਼ਿੰਦ ਦੇ ਦੇ ਦੇ ਪ	355 54 56 56 59 60 78 1166 226 226 226 226 217 77 77389 M						
PRT; 1196 AA. (ted) sequence update) annotation update) oor [Includes: Beta-amylase (EC 3.2.1.2);	TLAAGGTAVWQYTTAVTAFILGHV 53	YGDYYGIPOY	DYLM-YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHI 239	smatches 188; Indels 142; Gaps 2 -LGSLGITALWLPPAYKGTSRSDVGYGVYDL 62  : : : : :   : : :  : :	BY SIMILARITY. BY SIMILARITY. CALCIUM 2 (BY SIM CALCIUM 2 (VIA CA SIMILARITY). CALCIUM 2 (BY SIM CALCIUM 2 (BY SIM CALCIUM 2 (BY SIM CALCIUM 2 (VIA CA SIMILARITY). CALCIUM 1 (BY SIM CALCIUM 1 (UP SIM CALCIUM 1						

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SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEC
STRAIN=72;
MEDLINE=87165765; PubMed=2435707;
Kawazu T., Nakanishi Y., Uozumi N., Sasaki T
Tsukagoshi N., Udaka S.;
"Cloning and nucleotide sequence of the gene
active fragments of the Bacillus polymyxa be
J. Bacteriol. 169:1564-1570(1987).
                    InterPro; IPR006589; Alpamyl cat sub.
InterPro; IPR006048; Alpha amyl cat.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR005085; CBM 25.
InterPro; IPR005085; CBM 25.
InterPro; IPR005046; Glyco_hydro_13.
InterPro; IPR006046; Glyco_hydro_14.
InterPro; IPR001554; Glyco_hydro_14.
Pfam; PP00128; alpha-amylase; 1.
Pfam; PP00128; alpha-amylase; 1.
Pfam; PP003423; CBM 25; 2.
Pfam; PF003423; GBM 25; 2.
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-gorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymyxa beta-amylase.";
Biochemistry 30:4594-4599(1991).
-!-FUNCTION: THE PRECURSOR PROTEIN
-!- PRODUCE MULTIFORM BETA-AMYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H., Tsukagoshi N., Udaka S.; Tsukagoshi N., Udaka S.; "A single gene directs synthesis of a precursor protein with betand alpha-amylase activities in Bacillus polymyxa."; J. Bacteriol. 171:375-382(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paenibacillus polymyxa
Bacteria; Firmicutes; I
NCBI_TaxID=1406;
                                                                                                                                                  EMBL; M15817; AAA85446.1; -.
EMBL; Y00150; CAA68344.1; -.
FIR; A29130; A29130.
HSSP; P36924; 1892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES MEDLINE=91215008; PubMed=1827035; Uozumi N., Mateuda T., Tsukagoshi N., Udaka S.; "Structural and functional roles of cysteine residue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87231094; PubMed=2438660;
Rhodes C., Strasser J., Friedberg F.;
Requence of an active fragment of B.
Nucleic Acids Res. 15:3934-3934(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89123046; PubMed=2464578;
Uozumi N., Sakurai K., Sasaki T.,
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: In the N-terminal section;
                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic lin
polysaccharides so as to remove successive maltose units f.
non-reducing ends of the chains.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                 SECRETION.
CATALYTIC ACTIVITY: Hydrolysis
                                                                                                                                                                                                                                                                                                                               glycosyl hydrolases.
SIMILARITY: In the C-terminal section;
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lyco_hydro_14; 1.
ALPHAAMYLASE.
BETAAMYLASE.
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; Paenibacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                polysaccharides
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D A 48 kDa ALPHA
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ALPHA-AMYLASE
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SMART; SM00632; Aamy; C; 1.

PROSITE; PS00506; BETA AMYLASE 1; 1

PROSITE; PS00679; BETA AMYLASE 2; 1

Multifunctional enzyme; Hydrolase;

Polysaccharide degradation; Repeat.
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YQYIAKLNYVRNN--
                                                            LDHSDIIGWTREGGTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDL--TGNRSDTV
                                                                                                                                                                                 DPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDY
                                                                                                                                                                                                                                                 TIKDVFGHDQSMRKIKDRYSDDRYYRDAQTNGV-FIDNHDVKRFLNDASGKPGANYDKW-
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C-SS: 5-FOLD DECREASE IN A
C-SV: 20-FOLD DECREASE IN A
C-SC: 60-FOLD DECREASE IN A
M -> MIGL (IN REF. 3).
N -> S (IN REF. 3).
S -> N (IN REF. 3).
E -> Q (IN REF. 3).
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Pred. No. 4.3e-14;
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KS (IN REF. 3).
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InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco-hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAMYLASE.
SMART; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase; Glycsignal; Multigene family.
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POTENTIAL.
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AM3A OR
P27932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Japonica M202; TISSUE=Btiolated leaf; MEDILINE=9139692; PubMed=1714318; Sutliff T.D., Huang N., Litts J.C., Rodriguez R. "Characterization of an alpha-amylase multigene Plant Mol. Biol. 16:579-591(1991).
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01-AUG-1992 (Rel. 23, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Alpha-amylase isozyme 3A precursor (E)
glucan glucanohydrolase).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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AMY1.2 OR AMY3A
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HSSP; P04063; 1AVA.
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TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue. DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Important for breakdown of endosperm
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CDGT BACS8
P17692;
01-AUG-1990
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SEQUENCE
                              amylase).
Bacillus sp. (strain B1018).
Racteria; Firmicutes; Bacillales, Bacillaceae;
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
             SEQUENCE FROM N.A.,
  MEDLINE=90147765;
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PubMed=1689153;
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CALCIUM 1 AND 3 (BY
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                                                     Bacillus
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CDGT_BACS8 STANDARD; PRT; 713 AA.

AC P17692;
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last sequence precursor (EC 2.4.1.19)
Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (Raw-starch-digesting amylase)
DE (Cyclodextrin-glycosyltransferase) (Raw-starch-digesting amylase)
DE (Cyclodextrin-glycosyltransferase) (Raw-starch-digesting amylase gene from RT Nucleotide sequence of the raw-starch-digesting amylase gene from RT Nucleotide sequence of the raw-starch-digesting amylase gene from RT PUCTION: This endo-type adsorbable amylase is capable to digest raw starch.
CC -i-PUCTION: This endo-type adsorbable amylase is capable to digest raw starch.
CC -i-CATALTATTC ACTIVITY: Degrades starch to cyclodextrins by formation CC -I-CATALTATTY Belongs to family 13 of glycosyl hydrolases.
CC -I-SUBCELLULAR IOCATION: Secreted.
CC -I-SUBCELLULAR IOCATION: Secreted.
CC -I-SUBCELLULAR IOCATION: Secreted.
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                                                                                              DAVKHIKESEEPDWLSYVRSQTGKPLETVGEXWSXDIVKL--HVYITKTDGTWSLEDAPL
                                                                                                                                                            SFAENGRLYD
                                                                                                                                                                            VDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRI
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 LEGALAFTLILAR
                   WFKPLAYAFILTRQEGYPCVFYGDYYGIPQY-----
                                                                             DAVKHMPFGWQKSFMAAVNNY--KPVFTFGE-WFLGVNEVGPENHKFANESGMSLLDFRF
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                                      AQKVRQVFRDNTDNMYGLKAMLEGSAADYAQVDDQ--
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                                                        -SKSGGAFDMRTLMTNTL-----MKDQPTLAVTFVDNHDT$PGQALQSWVDP
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CALCIUM 1 (BY SIMILARITY).
CALCIUM 1 (VIA CARBONYL OX:
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Pred. No. 5,2e
30; Mismatches
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YYGTEQYMSGGTDPDNRARIPSFSTSTTAYQVIQKI
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(BY SIMILARITY).
(BY SIMILARITY).
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                                        --VTFIDNHDMERFHASNANRRK
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                     -NIPSLKS-----
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RESULT 11

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CDGU BA

CDGU BA

CDGU BA

CDGU BA

COYCLOM

DE CYCLOM

DE CYCLOM

DE CYCLOM

COC NCBL T

RA SEQUEN

RA KANK R

RA LAWSONE

RA KANK R

RI Glycos

RI Gepend

RI GPycos

RI GEPEN

RA KANK R

RI GEPEN

RA KOSEPEN

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RA ROZEPEN

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specificity.";
Biochemistry 35:4241-4249(1996).
Ci- CARLLYTIC ACTIVITY: Degrades starch to cyclodextrins by of a 1,4-alpha-D-glucosidic bond.
Ci- COPACTOR: Binds 2 calcium ions per subunit.
Ci- SUBUNIT: Monomer.
Ci- SUBUNIT: May consist of two protein domains: the one in terminal side cleaves the alpha-1,4-glucosidic bond in terminal side cleaves the alpha-1,4-glucosidic bond in the other in the C-terminal side catalyzes other activiticaliding the reconstitution of an alpha-1,4-glucosidic for cyclizing the maltooligosaccharide produced.
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p43379;
p1-307-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence updi
10-OCT-2003 (Rel. 42, Last annotation updi
Cyclomaltodextrin glucanotransferase pro
(Cyclodextrin-glycosyltransferase) (CGT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=251;
MEDLINE=96094317; PubMed=7493956;
MEDLINE=96094317; PubMed=7493956;
Knegtele R.A.A., Strokopytov B., Penninga D., Faber O.G.,
Knegtelle R.A.A., Dijkhuizen L., Dijkstra B.W.;
Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
"Crystellographic studies of the interaction of cyclodextrin
"Crystellographic studies of the interaction of cyclodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus circulans.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                               STRAIN=251;
MEDLINE=96264806; PubMed=8672460;
MEDLINE=96264806; PubMed=8672460;
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Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dij
"Nucleotide sequence and X-ray structure of cyclodextrin
glycosyltransferase from Bacillus circulans strain 251 ir
                                                                                                                                                                                                                                                                             Strokopytov B., Knegtel R.M.A., Penninga D., Ro
Dijkhuizen L., Dijketra B.W.;
"Structure of cyclodextrin glycosyltransferase
maltononaose inhibitor at 2.6-A resolution. Imp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penninga D., van der Veen B.A., knegtel R.M.A., van
Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhizen
"The raw starch binding domain of cyclodextrin glyco
from Bacillus circulans strain 251.";
J. Biol. Chem. 271:32777-32784(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyltransferase from Bacillus circulans substrates and products.";
J. Biol. Chem. 270:29256-29264(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97115811; PubMed=8955113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dependent crystal form.";
J. Mol. Biol. 236:590-600(1994).
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ise precursor
(CGTase).
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD 4.
InterPro; IPR002044; CBD 4.
InterPro; IPR002046; GlyCo hydro_13.
InterPro; IPR00210; IPT TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00128; alpha-amylase_C; 1.
Pfam; PF00666; CBM_20; 1.
Pfam; PF00666; CBM_20; 1.
Pfam; PF00666; CBM_20; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X78145; CAA55023.1; -.
PIR; A58800, A58800.
PDB; 1CGG; 08-MAR-95.
PDB; 1CGW; 27-FEB-95.
PDB; 1CGW; 27-FEB-95.
PDB; 1CGW; 07-FEB-95.
PDB; 1CXF; 15-DEC-95.
PDB; 1CXF; 15-DEC-95.
PDB; 1CXI; 15-DEC-95.
PDB; 1CXI; 15-DEC-95.
PDB; 1CXI; 15-DEC-95.
PDB; 1CXI; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1DXC; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 03-SEP-99.
PDB; 1CXI; 16-DAN-00.
PDB; 1CXI; 16-DAN-02.
PDB; 1CXI; 16-DAN-02.
PDB; 1CXI; 16-DAN-02.
PDB; 1CXI; 13-DAN-92.
PDB; 1CXI; 13-DAN-93.
PDB; 2CXG; 114-OCT-98.
PDB; 2CXG; 114-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
Transferase; GALL COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR 
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  Glycosyltransferase; Calcium-binding; Signal;
  NUCLEOPHILE.
PROTON DONOR.
SUBSTRATE BINDING.
CALCIUM 1. (VIA CARB
CALCIUM 1.
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CALCIUM 1.
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                            UM 1.
UM 1 (VIA CARBONYL OXYGEN).
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UM 1.
UM 2.
UM 2 (VIA CARBONYL OXYGEN).
UM 2 (VIA CARBONYL OXYGEN).
UM 2 (VIA CARBONYL OXYGEN).
                                         Query Match 10.5%; Sc
Best Local Similarity 24.8%; Pr
Matches 138; Conservative 77;
                                        Score 300; DB 1;
Pred. No. 7.2e-14;
77; Mismatches 200
       200;
                      Length 713;
       Indels 142;
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Gaps

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120 56 64 N

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01-MAR-1989 (Rel. 10, Created)
01-JUL-1993 (Rel. 26, Last sequence update).
10-CCT-2003 (Rel. 42, Last annotation update).
Cyclomaltodextrin glucanotransferase precurso
                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.

MEDLINE=89036108; PubMed=29772812;

Kaneko T., Hamamoto T., Horikoshi K.;

"Molecular cloning and nucleotide sequence of the cyclomaltodextrin glucanotransferase gene from the alkalophilic Bacillus sp. strain no
                                                                                                                                                                                                                                                                           Bacillus sp. (bull
teria; Firmicutes;
                                                                                                                     SEQUENCE OF 1-586 FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Cyclodextrin-glycosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 VDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRI
                                                                                                                                                    Microbiol. 134:97-105(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAFDGTCTN-LRLYCGGD---WQGIINKINDGYLTGMGVTAIWISQPVENIYSIINYSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVKHIKFSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKL--HNYITKTDGTMSLFDAPLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATPTIGHVGPMMAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTSLPQGS------YNDVLGGLLNGNTLSVGSGGAASNFTLAAGGTAVWQYTA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITDGPGGSKWMYVGKQHAGKVFYDLTGN--RSDTVTINSDG-WGEFKVNGGSVSVW-VPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKVRQVFRDNTDNMYGLKAMLEGSAADYAQVDDQ----VTFIDNHDMERFHASNANRRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGT------EKPGSGLAAL
                                                                                                                                                                                                                                                                                                       (strain 38-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALAFTLT-SRGVPAI----YYGTEQYMSGGTDPDNRARIPSFSTSTTAY
                                                                                                                                                                                                                                                                                          Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TTENGIYKNLYDLADLNHNNSTVDVYLKDAIKMWLD-LGIDGIRMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538
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                                                                         glucanotransferase
strain No. 38-2.";
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                                               formation
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                                                                                         Query Match
Best Local S
Matches 127
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InterPro; IPR006048; Alpha amyl C.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR002044; CBD 4.
InterPro; IPR002046; Glyco hydro 13.
InterPro; IPR007110; Ig_like.
InterPro; IPR007999; IPT TIG.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF00686; CBM 20; 1.
Pfam; PF00686; CBM 20; 1.
Pfam; PF00683; TIG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
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PYCDOm; PD001568; CBD 4; 1.
SMART; SM00642; Aamy, 1.
SMART; SM00632; Aamy_C; 1.
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EMBL; D00129; BAA00077.1; -.
HSSP; P05618; 1PAM.
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                                                                                             al Similarity
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                                WQGIINKINDGYLTGMGITAIWISQPVENIYSVINYSGVHNTAYHGYWARDFKK---TNP
 KYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQI
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CALCIUM 2 (BY SIMILARITY).
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CALCIUM 1 (BY S:
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                                                                                         Score 286.5; DB 1
Pred. No. 6.5e-13;
5; Mismatches 190
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NCBI\_TaxID=1412;

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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor
                               This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90174931; PubMed=2137908;
Hill D.E., Aldape R., Rozzell J.D.;
"Nucleotide_sequence_of_a cyclodextrin glucosyltransferase
                                                                                                                                                                                                                           MISCELLANBOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE OI
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BON
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
                                                                                                                                                                                                                                                                                                                                                    A, from Bacillus licheniformis.";
leic Acids Res. 18:199-199(1990).
CATALYTIC ACTIVITY: Degrades Earch to
of a 1,4-alpha-D-glucosidic bond.
COFACTOR: Binds 2 calcium ions per subu
SUBUNIT: Monomer.
                                                                                                                                                                                                      SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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pfam; pr02806; alpha-amylase; 1.

pfam; pr02806; alpha-amylase_C; 1.

pfam; pr00886; CBM 20; 1.

pfam; pr01833; TIG; 1.

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SMART; SM00632; Aamy; 1.
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SIGNAL 1
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0; IPR006048; Alpha amyl cat.
0; IPR006047; Alpha amyl cat.
0; IPR002044; CBD 4.
0; IPR006046; Glyco hydro 13.
0; IPR00710; Iglike.
0; IPR0072909; IPT_TIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                  TNTAYHGYWARDFKKTNPY------FGTMTDFQNLVTTAHAKGIKIIIDFAPNHTSP
  SGMSLLDFRFNSAVRNVFRDNTSNMYALD--SMLTATAADYNQVNDQ----VTFIDNHDM
                                                                                                                                                                                                             RKLSRIYKFRGIGKAWDWEVDTENGNYDYLM-YADLDMDHPEVVTELKNWGKWYVNTTNI
                                                                                                                                                                                                                                                                                              ADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APFNGTMMQYFEWYLPDDGTLWTKVANEANN--LSSLGITALWLPPA-----YKG-
                                        --MSL----FDAPLHNKFYTASKSGGAFDMRTLMTNTL-----MKDQPTLAVTFVDNHDT
                                                                                 DGIRVDAVKHMPQGWQKNWMSSIYAH -- KPVFTFGEWF ---
                                                                                                                            DGFRLDAVKHIKFSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGT-----
                                                                                                                                                                                                                                                      AMETDTSFAENGKLYDNGNLVGG------YTNDTNGY----FHHNGGSDFS--
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CALCIUM 1 (I
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BY SIMILARITY.
BY SIMILARITY.
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
                                                                                                                                                                       -TLENGIYKNLYDLADLNHNNSTIDTYFKDAIKLWLD-MGV
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Pred. No. 7.
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(BY SIMILARITY)
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454 442 405 386 365 333 310 277 256 219

488

RESULT 13
CDGT\_BACLI
ID CDGT\_BACLI

P14014;

STANDARD;

PRT;

718

cgtA, fr Nucleic

Bacillus licheniformis. Bacteria; Firmicutes; E

CBI\_TaxID=1402;

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CAA33763.1;

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197 195 138

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RESULT 14
CDGT_BACSO
ID CDGT_B
          EMBL; M17366; AAA22308.1; -
PIR; A26678; ALBSG1.
PDB; 1D7F; 17-MAR-00.
PDB; 1DED; 07-APR-00.
PDB; 1175; 11-APR-01.
PDB; 1PAM; 11-JAN-97.
                                                                                                                                                                                                                                                                                                                                                                                                P056T8;

01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation updat
Cyclomaltodextrin glucanotransferase precur
(Cyclodextrin-glycosyltransferase) (CGTase)
                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=87308036; PubMed=2957361;

Kimura K., Katacka S., Ishii Y., Takano T., Yamane K.;

Kimura K., Katacka S., Ishii Y., Takano T., Yamane K.;

Kimura K., Katacka S., Ishii Y., Takano T., Yamane K.;

"Nucleotide sequence of the beta-cyyclodextrin glucanotransferase gene of alkalophilic Bacillus sp. strain 1011 and similarity of its amino acid sequence to those of alpha-amylases.";

J. Bacteriol. 169:4399-4402(1987).
                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;

"X-ray structure of cyclodextrin glucanotransferase from alkalophilic Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A resolution.":
                                                                                                                                                                                                                                               resolution.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1410;
                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp. (strain ]
Bacteria; Firmicutes;
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IPR006589; Alp_amyl_cat_sub
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; Bacillales; Bacillaceae;
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    Transferase; G
3D-structure.
SIGNAL
CHAIN 2
   PRINTS;
ProDom;
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InterPro;
InterPro;
InterPro;
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InterPro; IPR002909; IPT TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C;
Pfam; PF02806; CBM_20; 1.
Pfam; PF01833; TIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00642; Aamy;
SMART; SM00632; Aamy
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PD001568; CBD_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR006048;
IPR006047;
IPR002044;
IPR006046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase; Calcium-binding; Signal;
    Alpha_amyl_C.
Alpha_amyl_cat.
CBD_4.
Glyco_hydro_13.
Ig-like.
IPT_TIG.
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AMYA_VIGMU
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Best Local Simi
Matches 135;
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P17859;
01-AUG-1990
01-AUG-1990
10-OCT-2003
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01-AUG-1990 (Rel. 15, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Alpha-amylase precursor (EC 3.2.1.1) (
glucanohydrolase).
                                                             TISSUE=Cotyledon;
MEDLINE=90332425; PubMed=2377468;
Yamauchi D., Minamikawa T.;
"Nucleotide sequence of cDNA for alpha-amylase
germinating Vigna mungo seeds.";
Nucleic Acids Res. 18:4250-4250(1990).
                                                                                                                                                                                                                                                                      Vigna mungo (Rice bean) (Black gram).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                           NCBI_TaxID=3915;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=94120017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465
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(1,4-alpha-D-glucan
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Best Local Similarity
Matches 103; Conserv
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EMBL; X73301; CAA51734.1; -.
PIR; S10514; S10514.
HSSP; P04063; 1AVA.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfan; PF00128; Alpha_amyl_ase; 1.
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SMART; S
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"Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
Plant Physiol. 103:1499-1495 (1993).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: Monomer (By similarity) 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carbohydrate
 266
                           289
                                                    207
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FTTKGILQAAVQGELWRLIDPNG----
                                                                            FPDWLSYVRSQTGKPLFTVGEYW---SY-----DINK--LHNYITKTDGTMSLFD
                                                                                                                                DWEVDTENGNYDYLMYADLDMDH--PEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSF
                                                                                                                                                            SRQDWGPSFICRDDTAYS-DGTGNNDS
                                                                                                                                                                                   RNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAW 185
                                                                                                                                                                                                              -----ASKYGSKNELKSLIAAFHEKGIKCLADIVINHRTAERKDGRGIYCIFEGGTPD
                                                                                                                                                                                                                                      FNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGG--ADGTEWVDAVEVNPSD
                                                                                                                                                                                                                                                                 LFQGFNWESSKKGGWYNSLKNSIPDLANAGITHVWLPP--PSQSVSPEGYLPGRLYDLD-
                                                   APS-ISKIYMEQTKPDFAVGEKWDSISYGQDGKPNYNQDSHRGALVNWVESAGGAITAFD
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                        ----APLHNKFYTASKSGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQS 340
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                                                                                                       -----AAPDIDHLNPQVQRELSEWMNWLKTEIGFDGWRFDFVK----GY
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46888 MW;
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CALCIUM 1 AND 3 (BY SIMILARITY).
15CAODABA3DB4656 CRC64;
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Search completed: May 3, 2004, 20:51:15

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Result
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Perfect score:
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      seq length: 0
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Aaw22523 Alpha-amy
Aaw23603 Alpha-amy
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Aaw3942 B. lichen
Aar81475 Wild type
Aaw14498 Bacillus
Aaw39742 B. lichen
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Aag65881 B. lichen
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B. lichen
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Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;

Bacillus licheniformis alpha amylase (mature protein).

25-MAR-2003 01-DEC-1995 AAR72447;

(revised) (first en

entry)

AAR72447 standard; protein; 483

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## ALIGNMENTS

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New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance.
                                                                              WPI; 1995-161790/21.
N-PSDB; AAQ88066.
                                                                                               Borchert TV,
Van Der Zee
                                                                                                                            08-OCT-1993;
02-FEB-1994;
                                                                                                                                             05-OCT-1994;
                                                                                                                                                                               Bacillus licheniformis.
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94DK-00000140
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AAG65881

Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PN field.)

Claim 6; Page 72; 105pp; English.

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AAW31404; 17-OCT-2003 11-MAY-1998

(revised) (first entry) AAW31404

standard; protein; 483

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Termamyl; alpha-amylase; enzyme engineering; protein engineering; liquefaction; saccharification; sweetener; textile desizing; detergent additive.

Bacillus licheniformis Termamyl alpha-amylase

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Matches 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 22; 37pp; English.
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                                                                          NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                                                                                                                     VFYGDMYGTKGDSQREIFALKHKIEFILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
                                                                                                                                                                                  GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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VOR
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                           VQR 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2666; ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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CC from: substrate specifically, binding or cleavage pattern; thermal considering considerion; C22 dependency and specific; stability towards concernation; C22 dependency and specific activity. The variant has one or CC entropy and specific activity. The variant has one or CC (bulkier amino acid) including 1201W, F, L; Y2030, 09K, L, E; F118, K, E; CC H105R, K, D, E, W, Y233D, K234I, E; T136R, K, D, E, F, Y102R, K, D, E; Y2030, 09K, L, E; F118, K, E; CC H105R, K, D, E, W, Y233D, K234I, E; T136R, K, M, D, E; L230H, K, I; CC H202; D100N, L; V101H, R, K, D, E, F1731B, K, E; CC H, D, E; V283H, D; F284H; D25R, K, D, E, F273R, K, D, E; L270R, K, CC H, D, E; V283H, D; F284H; D25R, K, D, E, K25K, R, D, B; L270R, K, CC H, D, E; V283H, D; F284H; D25R, K, M, T, L, D, E; V290R, E, K; CC H, D, E; V283H, D; F284H; D25R, K, M, T, D, D; X290R, E, K; CC H312R, K, D, E; F333H; D325R, M326K, H, D, E; L230R, K, M, E, D; E; V293R, E, K; T33BD, E; T33BD, E; T33BD, E; T33BD, E; T33BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD, E; T38BD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Termamyl-like alpha-amylase variants with improved properties - e. increased stability at low pH and low calcium, useful as detergent additives and in industrial starch processing e.g. liquefaction.
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Sequence 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bisgard-Frantzen
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in at least one property selec
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Query Match Best Local Similarity Matches 483; Conserv

100.0%; ilarity 100.0%; Conservative 0

Score 2666; DB 2; Pred. No. 1.7e-224; Mismatches

Length Indels

483;

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Claim 38; Page 82-84; 115pp; English

New Termamyl-like alpha-amylase variants

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14-JUL-1998;
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                                                                                                                                                                                                                                                Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction;
                                                                                                                                                                                                                                                                             Bacillus licheniformis alpha-amylase protein.
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Matches 483
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                                                              Alpha-amylase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 483 AA;
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                                                                  NSGLAALITDGPGGAKRNYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
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Pred. No. 1.7e-224;
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                                                                                                                                                 This sequence represents the parent sequence for new variants of a parent Termamyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1998;
                                                                                                                        Sequence
                                                                                                                                                                                                                                             Claim 1; Page 67-68; 93pp;
                                                                                                                                            sweeteners or ethanol)
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                   LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGÅDÅTEDVTÅVEV
                                                        ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                         483 AA;
                                          ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
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The present sequence is a parent alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The enzyme is commercially available as Termamyl. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by sitedirected mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial

Variant of parent termamyl-like alpha amylase useful for washing, tdesizing and starch liquefaction, comprising alterations in one or solvent exposed amino acid residues.

Claim 8; Page 58-59; 80pp; English.

Svendsen A,

Kjaerulff

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Bisgard-Frantzen

H,

G

2000-387777/33.

AAA48483.

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                                                                                                                                                                                                                                                        Termamyl-like alpha-amylase; variant; starch liquefaction; detergent composition; laundry cleaning composition; ethano dish washing cleaning composition; hard surface cleaning coindustrial ethanol production; textile desizing.
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CC This sequence represents a termamyl-like alpha amylase. The invention CC relates to a variant (I) of parent Termamyl-like alpha-amylase comprising CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52, CC D53, V54, G57, G108, A111, S168 and M197. The alterations in (I) CC are independently an insertion of an amino acid downstream of the amino CC acid which occupies the position or deletion or substitution of the amino CC acid which occupies the position with a different amino acid. The variant CC has alpha-amylase activity. (I) or compositions containing it are useful in starch liquefaction, in detergent compositions such as laundry, dish CC washing and hard surface cleaning compositions, ethanol production such as fuel, drinking and industrial ethanol production, desizing of creating a fabrics or garments. (I) exhibits a reduced capability of CC cleaving a substrate specificity and/or improved specific activity relative to the parent alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen (
Kjaerulff
                                                                                                                                                                                                                                                                                                                                                                                 New variants of parent Termamyl-like alpha-amylase, useful in starch liquefaction, in detergent compositions and in ethanol production, exhibit altered cleavage pattern relative to the parent.
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S Query Match Best Local S Matches 483 483; Similarity 100.0%; ilarity 100.0%; Conservative 0 0 Score 2666; Pred. No. 1.7 0; Mismatches ; DB 4; 1.7e-224; es 0; Length Indels 483; 0 0

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                                                                                                                                                                  Matches 483;
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Best Local :
                                                                                                                                                                                                                                                        The present invention describes a variant of a parent termamyl-like alpha -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more positions of a group of 31 possible amino acid positions. The alteration in (I) may be at Arg28, Arg118, Asn174, Arg189, Gly182, Asg183, Gly184, Asn195, Met.202, Tyr298, Asn299, Lys302, Ser303, Asn306, Arg310, Asn314, Arg320, His324, Glu345, Tyr296, Arg400, Trp439, Arg444, Asn445, Lys466, Gln449, Arg458, Asn471, or Asn484. (I) can be used for washing and/or dishwashing, textile desizing, and starch liquefaction. (I) is useful as a component in hard surface cleaning detergent composition, and for producing sweeteners and ethanol from starch. (I) has altered solubility, preferably increased solubility, in particular under washing, dish washing or hard surface cleaning conditions. The present sequence represents a Bacillus licheniformis termamyl-like alphamylase which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000;
15-MAR-2000;
23-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel variant of parent termamyl-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.
                                                                                                                                                                                                                                 Sequence 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 142-143; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     washing; sweetener; ethanol; starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1; variant; mutant; enzyme; protein co-ordinate data; cleaning; dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. licheniformis termamyl-like alpha-amylase protein
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 DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 180
                                                            LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                     LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV
                                                                                                                             ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                                                                  Conservative
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2000US-0189857P.
2001DK-00000303.
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Pred. No. 1
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.7e-224;
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                             481 VQR 483
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                                                           NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                                                                                                                                                                                                   GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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VQR 483
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                                                                                                                           VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
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AAU12152 standard; protein; 483 AA.

09-APR-2002 (first entry)

Bacillus TERMAMYL alpha-amylase.

amylopectin; limit dextrin; NOVAMYL TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing; starch liquefaction; ethanol production; hard surface cleaner; swe

Bacillus licheniformis.

WO200188107-A2

22-NOV-2001

10-MAY-2001; 2001WO-DK000323.

12-MAY-2000; 2000DK-00000779.

(NOVO ) NOVOZYMES AS

Svendsen A, Jorgensen G, Nielsen BR;

WFI; 2002-106123/14. N-PSDB; AAS20025.

New variant of parent Termamyl-like alpha-amylase for use as a component in washing and dishwashing compositions, for textile desizing, for starc liquefaction, and for producing sweeteners and ethanols from starch. for starch

Claim 5; Fig 1; 84pp; English.

ARESULT 10
AAU12152
ID AAU122
XX AAU12
AC AAU12
XX O9-AP
XX TERMA
XW Starc
XX AW10
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XX MAU10
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X The invention relates to a variant of parent TERMAMYL-like alpha-amylase comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339, or at position 234, where the variant has alpha-amylase activity and each position corresponds to a position of a parent Termamyl-like alpha-amylase sequence having a Bacillus licheniformis alpha-amylase sequence of 483 amino acids, given in specification. The variant alpha-amylase, a detergent additive comprising the variant or a detergent composition comprising the variant, is useful for washing and/or dishwashing or textile desizing. The alpha-amylase is useful for starch liquefaction or ethanol production and as a component in a hard surface cleaning

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DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK

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RESULT 11
AAE26534
ID AAE26534
XX AAE26
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DT 13-DE
DE Bacil
XX Alpha
KW dishn
KW laum
KW laum
KW laum
KW Sweet
XX Sweet
XX WO200
XX WO200
XX X
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Matches 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                     Alpha amylase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1; dishwashing; textile desizing; detergent; paper; starch liquefaction; laundry; alcohol production; ethanol production; pulp; beer; brewing;
                                                                                                                                                                                                                                                                                AAE26534
                                                                                                 Bacillus licheniformis
                                                                                                                          sweetener;
                                                                                                                                                                                               Bacillus licheniformis alpha-amylase
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Pred. No. 1.7e-224;
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12-OCT-2001; 2001WO-DK000668

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23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to KSM-K36 or KSM-K38 variant of parent alpha-amylases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from Bacillus. The variants have alpha-amylase activity and exhibit an amino sold alteration such as an insertion, deletion or substitution of the parent alpha-amylase. The variants are useful for washing and/or dishwashing, textile desizing, starch liquefaction and alcohol production, washing textile desizing, starch liquefaction and alcohol production, particularly ethanol production. They are also useful as components in detergents for e.g. laundry, dishwashing and hard surface cleaning detergent compositions, in pulp and paper production, in beer making or brewing and in production of sweeteners. The present sequence is Bacillus licheniformis alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \kappa_{SM}-\kappa_{36} or \kappa_{SM}-\kappa_{38} variant from Bacillus for cleaning dishes, textile desizing, starch liquefaction and ethanol production has alpha-amylase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified alpha-amylase derived Termamyl-like alpha-amylase, which maltodextrin or glucose syrup.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2000; 2000DK-00000917.
20-JUN-2000; 2000US-0212852P.
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                                                                                                                                                 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV
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12-SEP-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                  Variant of parent Termamyl-like alpha amylase, useful in detergent compositions, for starch liquefaction, ethanol production, washing dish washing, and textile desizing.
                                                                      This invention relates to variants of a parent Termanyl-like amylases. These are used for starch liquefaction, ethanol prodetergent, and textile desizing. The amylases have altered sparticularly at high temperatures from 70-120plusoC and low range from pH 4.0-6.0. The present sequence is a termamyl-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus licheniformis
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textile desizing; detergent;
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                                                                                                                                                                                                                           Claim
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; 2001DX-0000655.
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Best Local Similarity
Matches 483; Conserv
                                                                                                                                                                                                                                                                           Synthetic.
unspecified
                                                                                                                                                                                                                                                                                                                              Allergen; allergy; self-oligomerising polypeptide; Termamyl; alpha-amylase; leucine zipper; detergent.
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16-OCT-1996
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                    23-NOV-1995;
                                                     30-MAY-1996.
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                                                                                                                                                                                        /label= Termamyl
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                         label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2666; DB 5;
100.0%; Pred. No. 1.7e-224;
tive 0; Mismatches 0;
                                                                                                                                                                        .489
                                                                                                                      Leucine_zipper
                                                                                                                                                         Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 AA
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Best Local Similarity 100.0%;
Matches 483; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 61-63; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 531
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          AAW22523 standard;
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DB; AAT33228.
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          protein; 630
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A polypeptide (AAR98007) is composed of Termamyl alpha-amylase, a linker derived from the IgG3 hinge domain and a leucine zipper from the GCN4 yeast transcription factor. It was produced by PCR amplification of the Termamyl gene and ligation of synthetic oligonucleotides (see also AAT33229-32) encoding the leucine zipper and linker. Upon expression in E.coli, using a vector including the pelB signal sequence, the Termamyl product self-oligomerised into a dimer that was secreted into the periplasm. The method constitutes an industrially applicable process for producing a biologically active polypeptide that self-oligomerises owing to the presence of leucine zippers, the enlarged size of the resulting polypeptide leading to a reduction in its allergenicity. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  odn. of self-oligomerising peptide(s) with reduced allergenicity - household and personal cleaning prods., and in food and feeds etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYDLGEFHOKGTVRTKYGTKGELOSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYDLGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLNGTLMQYFBWYMANDGQHWRRLQNDSAYLABHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANBLOLDGFRLDAVKHIKFSF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 180
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                                                                                                                                                                                                 VFYGDMYGTKGDSQREIPALKHKIEFILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
                                                                                                                                                                                                                                                                                      GYDWRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRDWVNHVREKTGKEMETVAEYWONDLGALENYLNKTNENHSVEDVPLHYQFHAASTQGG
                                              NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWDWEVSNENGNYDYLNYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF
NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY
                                                                                                                                              KGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA
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Pred. No. 1.9e-224;
Mismatches 0;
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Matches 483; Conserv
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Peptide
                                                                                                                                                                                                                     This protein sequence comprises a hybrid enzyme in which Bacillus licheniformis alpha-amylase (Termamyl) signal peptide is linked to the cellulose binding domain (CBD) of cellulomonas fimi CenA, which is further linked to mature Termamyl polypeptide. The CDB-Termamyl fusion has been expressed and secreted as an approx. 85 kDa protein in Bacillus subtilis PL2306 transformants. A claimed process for desizing cellulose-containing fabric or textile comprises treating the fabric or textile with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic enzyme linked to a CBD. The process gives improved enzyme performance by modifying the enzyme so as to increase its affinity for cellulosic fabric. A desizing composition suitable for use in the process comprises the enzyme hybrid and a wetting agent. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desizing; cellulose; fabric; enzyme hybrid; Termamyl; alpha-amylase; cellulose binding domain; CenA; Bacillus licheniformis; Cellulomonas fimi; protein secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desizing cellulose-containing fabric or textile using an enzyme hybrid which comprises a catalytically active amino acid sequence of a noncellulolytic enzyme linked to an amino acid sequence comprising a cellulose binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402610/37.
N-PSDB; AAT77063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Von Der Osten C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis. Cellulomonas fimi; stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase-CenA cellulose binding domain hybrid enzyme.
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08-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 60; 72pp; English.
                                                                                                                                                                                 Sequence 630 AA;
                                                                                                                                                                                                                standardise OS field)
 208
                                                            148
                     61 LYDLGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
                                                                                         Н
                                                                                    ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                          ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
                                                                                                                        Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96DK-00000093.
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/note= "CBD (aa29-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Sig_peptide
/note= "Termamyl signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bjornvad M,
                                                                                                                   100.0%; Score 2666; DB 2;
100.0%; Pred. No. 2.5e-224;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rasmussen
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                                                                                                                        Indels
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VQR 630	VQR 483	NSGLAALITDGPGGAKHMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY 627	42\\NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480	VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 567	VFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420	GYDMRKLLNGTVVSKIPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 507	GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 360	LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 447	LRDWVNHYREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300	AWDWEVSNENGNYDYLMYADIDYDHEDVAAEIKRWGTWYANBLQLDGFRLDAVKHIKFSF 387	AMDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF 240	DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK 327	DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRXLNRIYKFQGK 180

Search completed: May 3, 2004, 20:50:29 Job time : 53.0521 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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Match Length
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sp_rodent:*
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sp_mammal:*
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O3L193
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O9SYP166
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Q81as4 bacillus me
Q81as4 bacillus an
Q81as54 bacillus an
Q81as3 bacillus st
Q81as5 bacillus st
Q81as6 bacillus st
Q9kwy6 bacillus st
P71034 bacillus st
P71034 bacillus st
P71034 bacillus st
Q93as6 bacillus sp
Q83as6 vibrio para
Q89ypl bacieroides
Q8657 bacillus ci
Q97q49 streptococc
Q86666 streptococc
Q86666 streptococc
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## ALIGNMENTS

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Q9RQT8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Raw starch digesting amylase precursor.
                                                                                                                                                                                                                                                                      signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Jeang C.L., Chen L.S., Chen M.Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF067563; AAF00567.1; -
HSSP; P06278; 1VJS.
                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0004556; F:alpha-amylase activity; I
GO; GO:0005975; P:carbohydrate metabolism;
InterPro; IPR006047; Alpha_amyl_cat_
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PFRINTS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Flexibacteraceae; Cytophaga.
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                                        NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
NGTMMQYFEWYVPNDGQQWNRLRTDAPYLSSVGITAVWTPPAYKGTSQADVGYGPYDLYD
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58
519 AA;
                                                                                                                                   nilarity (78.5%;)
Conservative (
                                                                                                                                                                                                57
519
58337/MW;
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                                                                                                                               Score 2061; DB 2;
Pred. No. 3.8e-134;
8; Mismatches 70;
                                                                                                                                                                                                                                                                  POTENTIAL.
RAW STARCH DIGESTING AMYLASE,
3E6E88A4DF98B163 CRC64;
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G0; G0:0004556; F: Alpha-amylase activity; IEA.
G0; G0:0016798; F: hydrolase activity, acting on g0; G0:0016798; P: carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006089; Alpha amyl cat.
InterPro; IPR006589; Alpha amyl cat.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINB=22608415; PubMed=12721630;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.;

"Genome sequence of Bacillus cereus and comparative analysis with the sequence of Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TYEMBLEE). 24, Created)
01-JUN-2003 (TYEMBLEE]. 24, Last sequence update)
01-OCT-2003 (TYEMBLEE). 25, Last annotation update)
Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
                                                                                                                                                                                                                         Glycosidase; Hydrolase; SEQUENCE 513 AA; 5830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus (strain ATCC 14579 /
Bacteria; Firmicutes; Bacillales; Bac
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                                                                                                      N
                                                                                                                                                              Similarity
LGEFQQKGTVRTKYGTKSELQDA1GSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA
                                                            NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD
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                                                                                                                                              Conservative
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58306 MW; 05C4611C4BFF9FF6 CRC64;
                                                                                                                                                              74.2%;
                                                                                                                                            Score 1947; D
Pred. No. 2.8e
17; Mismatches
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Bacillaceae;
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ova N., Lapidus A.,
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Best Local Similarity 72.3
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-amylase.
Bacillus megaterium.
Bacteria; Firmicutes; B
NCBI_TaxID=1404;
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Q9AQ54;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004556; F:alpha-amylase activity; GO; GO:0005975; P:carbohydrate metabolism; InterPro; IPR006047; Alpha_amyl_cat. InterPro; IPR006047; Alpha_amyl_cat_sub. Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF220440; AAK
HSSP; P06278; 1VJS.
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Kim Y.B., Lee B.N.,
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2000)
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                                                                                                                                                                                                                                                                                                                                                             SM00642; Aamy; 1.
533 AA; 60557 MW; 789CECD6A19C7DDE
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                                                                                                                                                                   LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of maltopentaose-producing amylase from
                                                            NRNQETSEEYQIKAWIDFRFPGRGNIYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA
                                                                                                                                                                                                                       NGTLMQYFEWYAPNDGNHWNRLRTDAENLAQKGITSVWIPPAYKGTTQNDVGYGAYDLYD
                                                                                                                                                                                                                                            NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGFYDLYD
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GEFNQKGTVRTKYGTKAQLKGAIDALHKKNIDVYGDVVMNHKGGADYTETVTAVEVDPS
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3 (TrEMBLrel.
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                Score 1946; DB 2;
Pred. No. 3.5e-126;
4; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Matches 339
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Q81YJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T. Melson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu K., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Helson W.C., Paterson J.D., Pop M., Khouri H.M., Weidman J.F., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., White O., Salzberg Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0004566; F:alpha-amylase activity; GO; GO:0005975; P:carbohydrate metabolism; InterPro; IPR006047; Alpha amyl cat. InterPro; IPR006589; Alpha amyl cat sub. Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE017035; AAP27311.1; -. TIGR; BA3551; -.
                                                                                                                                                                                                                                                                                                                                                                             Complete proteomé.
SEQUENCE 513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          closely related bacteria.";
Nature 423:81-86(2003).
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NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDBSRKISRIFKFRGEGKA
                                                                                                  LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA
                                                                                                                                                                          NGTLMQYFEWYAPSDRNHWNRLRTDAENLAQKGITSVWIPPAYKGTTQNDVGYGAYDLYD
                                                                                                                                                                                                             NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD
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Pred. No. 5.3e-124;
7; Mismatches 93;
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Best Local Similarity
Matches 323; Conserv
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GO; GO:0005975; P:carbohydrate metabolism; IE
InterPro; IPR006047; Alpha-amyl_cat
InterPro; IPR0060489; Alp_amyl_cat sub.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR001010; ALPHANYLASE.
SNART; SN00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amylase.
Bacillus sp.
Bacteria; Fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Improved thermostability of a Bacillus alpha-amylase an arginine-glycine residue is caused by enhanced calc Biochem. Biophys. Res. Commun. 248:372-377(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB008763; BAA32431.1; -. HSSP; P06278; IVJS.
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01-JUN-2003
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Igarashi K., Hatada Y., Ikawa K.,
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STRAIN=KSM-1378,
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SM00642; Aamy; 1.
SM00642; Aa; 58841 MW; D90A8C90ECC182F8
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AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                                         NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKI-SRIFKFRGEGK
                                                                                                                                                       LGEFNOKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRS
                                                                                                                                                                                                                                               NGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGAYDLYD
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ESTRAINATCC 31195;

CANADINATIC AC.R., Fernandes E., Pueyo M.T.;

da Silva A.C.R., Fernandes E., Pueyo M.T.;

Labmitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF032864; AAB86961.1; -.

FIR; A54541; A54541.

FIR; A693484; AAB86961.1; -.

FOG: 00:004556; F:alpha-amylase activity; IEA.

GO; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR006047; Alpha-amyl_cat.

InterPro; IPR006047; Alpha-amyl_cat.

InterPro; IPR006046; GlyGo_hydro_I3.

FIAM; PR00128; alpha-amylase; 1.

R PRINTS; PR00110; ALPHAMYLASE.

SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;
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Best Local S
Matches 315
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01-JAN-1998
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Bacteria, Firmicutes; Bacillales;
NCBI_TaxID=1422;
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                                                    WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFL
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Last sequence
Last annotation
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Pred. No. 7.8
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EMBL; Y17557; CAB93517.1; -.

PIR; A55491, A54541

HSSP; p06278; 1VJS.

GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on gl:
GO; GO:0016798; F:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha-amylacat.
InterPro; IPR006047; Alpha-amylacat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PP00128; alpha-amylase; 1.
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01-CCT-2000 (TrEMBLrel. 15, Last sec
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01-CCT-2003 (TrEMBLrel. 25, Last and
Alpha-amylase (EC 3.2.1.1)
Badillus stearchtermophilus
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SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
SEQUENCE 549 AA; 62582
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                                                                        RDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGG
                                                                                                                WDWEVDTENGNYDYLMYADLOMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFF
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Last annotation
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Pred. No. 9.2e-
57; Mismatches
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nes 103;
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549; ş

Gaps

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Best Local Sim
Matches 314;
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C STRAIN=MK 716;

C STRAIN=MK 716;

A Sidhu G.S., Chakarbarti T.;

A Sidhu G.S., Chakarbarti T.;

Molecular cloning and expression of the gene encoding for "Molecular cloning amylase of a thermophilic bacterial iso submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.

T thermostable alpha-amylase activity; IEA.

R EMBL, UT5445; ALBI8785.1; -.

R HSSP, P06278; IVJS.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR006047; Alpha_amyl_cat.

R InterPro; IPR006047; Alpha_amyl_cat sub.

R InterPro; IPR006048; Glyco_hydro_13.

R Pfam; PF00128; alpha-amylase; 1.

R PRINTS; PR00110; ALPHAANYLASE.
                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-amylase precursor.
Bacillus sp. MK 716.
Bacteria; Firmicutes; Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                    WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFL
                                                                                                                                                                          NRNQETSEEYQIKAWTDFRFFGGGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA
                                                                                                                                                                                                                         LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA
FOMETIMENTEMEDQPTEAVTEVDNHDTEPGQALQSWVDPWFKELAYAFILTRQEGYPCV
                                                                         RDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGG
                                                                                                                                                      DRNOEISGTYOIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA
                                                                                                                                                                                                         LGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPS
                                                                                                                                                                                                                                                           NGTWMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTTTSDGWGEFKVNGGSVSVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPGV
                        YDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV
                                                     PDWLSYVRSQTCKPLFTV
                                                                                                      WDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFF
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521 A
59311 MW;
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Last sequence upo
Last annotation
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Pred. No. 1.6e-113;
7; Mismatches 104;
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ALPHA-AMYLASE.
; 5612A88596D922E1 CRC64;
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; UZ2045; AAA63900.1; -.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0004576; F:alpha-amylase activity, acting on glycosyl bonds; IEA.

GO; GO:0006477; F:purine nucleosidase activity; IEA.

DR GO; GO:0008477; F:purine nucleosidase activity; IEA.

GO; GO:0008975; P:carbohydrate metabolism; IEA.

Interpro; IPR006047; Alpha_amyl_cat_sub.

Interpro; IPR006047; Alpha_amyl_cat_sub.

Interpro; IPR006048; CBD_4.

DR Interpro; IPR006046; GBD_4.

DR Interpro; IPR006046; GBD_4.

DR Interpro; IPR006046; GBD_4.

DR Pfam; PF00128; alpha-amylase; 1.

DR Pfam; PF00128; alpha-amylase; 1.

DR Pfam; PF001266; CBM_20; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

PRINTS; PR00110; ALPHAMYLASE.

PRODOm; PD001566; CBD_4; 1.

DR SMART; SM00642; Aamy; 1.

SM SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
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Matches 313
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Q5922;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, I
01-JUN-2003 (TrEMBLrel. 24, I
Alpha-amylase (EC 3.2.2.1).
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STRAIN=TS-23;
Lin L.-L., Chu W.S.,
Submitted (MAR-1995)
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Bacteria; Firmicutes;
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  335
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313; Conservat
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                                                                                                                                                                                                   AWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSF
                                                                                                                                                                                                                                                                                                                                               DLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNP
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                                                                                                                                 LRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGG
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  YFDMRYLLNNTLMKDQPSLAVTLVDNHDTQPGQSLQSWVEPWFKPLAYAFILTRQEGYPC
                                                    GYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                        FPDWLTYVRNQTGKNLFAVGEFWSYDVNKLHNYITKTNGSMSLFDAPLHNNFYTASKSSG
                                                                                                                                                                                                                                                                                                              SNRNOETSGTYQIQAWTKFDFFGRGNTYSSFKWRWYHFDGTDWDESRKLNRIYKFRSTGK
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Last
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Pred. No. 1.6e-112;
58; Mismatches 105;
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VFYGDMYGTKGTSPK-EIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSA

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Query Match
Best Local S
Matches 287
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01-DEC-2001
01-JUN-2003
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Bacteria; Firmicutes;
NCBI_TaxID=129736;
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67; Mismatches
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Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Tuncet Sequence of Vibrio parahaemolyticus: a pathogenic mechanism

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Lancet Sequence of Vibrio parahaemolyticus: a pathogenic mechanism

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

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Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

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Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Lancet Sequence of Vibrio parahaemolyticus: a pathogenic mechanism

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Hattori M., Iida T., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,

Yasunaga T., Hattori M., Kubota Y., Kimura S.,

Yasunaga T., Hattori M., Yasunaga K., Uda T., Kimura S.,

Yasunaga T., Hattori M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Yokoyana K., Vokoyana K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Luba M., Yasunaga K., Yasunaga K., Yasunaga 
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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Best Local S
Matches 244
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MEDLINE=22550858; PubMede12663928;

M. U. J. Bjursell M.K., Himrod J. Deng S., Carmichael L.K.,

A. Yu. J. Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron sym

Science 299:2074-2076 (2003).

EMBL, AB016946; AA079795.1; -.

R GO: GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR006047; Alpha-amyl_cat.

InterPro; IPR006047; Alpha-amyl_cat.

R Pfam; PF00128; Alpha-amyl_ase; 1.

R SMART; SM00642; Aamy; 1.
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Q89YP1;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase
BT4690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 481 AA;
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STRAIN=VPI-5482 /
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Bacteria; Bacteroidetes; Bact
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                                               422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WDWEVSSENGNYDYLMYADVDYDHDDVVABTKKWGIWYANELSLDGFRIDAAKHIKFSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD
                              SGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
                                                                                                                              FYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAAK
                                                                                                                                                                                                                                                                                                                                                                  RDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGG
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SGLVFLMSNDEAGSKIMSLGEKHKGEVWHEITGSISEEITLDEEGNGEFSVESRNLAVW
                                                                                                                                                                                                             YDLRDILKDTLVEHHPDLAVTIVDNHDTQRGSSLESNVEDWFKPLAYGLILLMKEGYPCL
                                                                                                                                                                                                                                            YDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV
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                                                                                                     EKSPHTR-IIDILLDARRKYAYGDQIEYFDHPSTIGFIRTGDEEHNG
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; Pred. No. 1.1e-85;
82; Mismatches 149; Indels
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RESULT Q03657 ID Q0 AC Q0 DT 01

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Q03657 Q03657; Q1-NOV-1996

(TrEMBLrel. PRELIMINARY;

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RESULT 14
Q97Q49
ID 097Q4
AC Q97Q4
DT 01-OC
DT 01-OL
DT 01-UL
DE Alpha
GN Strag
OC Streg
OC Streg

Alpha-amylase. SP1382.

Q97Q49 Q97Q49; 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2003 (TrEMBLrel. 24,

Created)
Last sequence up
Last annotation

sequence update)

update)

484

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Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales;

Streptococcaceae;

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01-JUN-2003
Amylase.
AMYE.
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Marcel T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat sub.
InterPro; IPR006686; Alp_camyl_cat sub.
InterPro; IPR0006046; Glyco_hydro_13.

Pfam; PF00128; alpha-amylase; 1.

PRINTS; PR00110; ALPHAAYILASE.
SMART; SW00642; Aamy; 1.
SMART; SW00642; Aamy; 1.
SMART; SW00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 0:0-0(0 EMBL; X60779; CAA43194.1; PIR; S15713; S15713. HSSP; P06278; IVJS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus circulans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0004556; F:alpha-amylase activity;
GO; GO:0005975; P:carbohydrate metabolism;
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NCBI_TaxID=1397;
                        422
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM' N.A
                                                                                                  FDLSKIFDDTLVQTHPTHAVTFVDNHDSQPHEALESWIGDWFKPSAYALTLLRRDGYPVV
                                                                                                                                                                                                                        WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFL
                                                                                                                                                                                                                                                            DRTKEISEPPEIEGWTKFTFPGRGDQYSSFKWNSEHFNGTDFDAREERTGVFRIAGENKK
                                                                                                                                                                                                                                                                             NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKA
                                                                                                                                                                                                                                                                                                                                 LGBFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPA
                SGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                      FYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAAK 421
                                                                                                                    KEFAAEMIRKRGQDFYIVGEFWNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLKGRD
                                                                                                                                                                               RDWVQAVRQATGKEMETVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGG
                                                                                                                                                                                                                                                                                                               LGEFDOKGTVRTKYGTKQELIEAIAECOKNGIAVYVDLVMNHKAGADETEVFKVIEVDPN
                                                                                                                                                                                                                                                                                                                                                                  NHTMMQFFEWHLAADGDHWKRLAEMAPELKAKGIDTVWVPPVTKAVSAEDTGYGVYDLYD
SGCAVVISNGDDGEKRMFIGEHRAGEVWVDLTKSCDDQITIEEDGWATFHVCGGGVSVW
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                    - PEPVDGKKEILDILLSARCNKAYGEQEDYFDHANTIGWVRRGVEEIEG
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Last annotation updat
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Pred. No. 2
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ed. No. 2.4e-78;
Mismatches 177;
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K MEDLINE=21357209; PubMedel1463916;

A Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

A Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

A Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

A Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

A Holtrapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

A Holtrapple E., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.

A McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.

A Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

A Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

T Complete genome sequence of a virulent isolate of Streptococcus

T pneumoniae.",

Science 293:498-506(2001).
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GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR0060589; Alp_amyl_cat_sub.
InterPro; IPR006046; Glyco_hydro_i3.
Pfam; PF00128; alpha-amylase; 1.
PFNINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
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PIR; G95160; G95160.
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SEQUENCE FROM N.A
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                                                                                                                                    AKSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSI
                                                                                                                                                                                                                CVFYGDYYGISGOYAQE--DFKEILDRLLAIRKDLAYGEONDYFDHANCIGWVRSGAEN-
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Pred. No. 7.3e-76;
(1; Mismatches 168;
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PRINTS; PROO110; ALPHAMYLASE.
SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase; Complete proteome.
404 AA: 55880 MW; DA511868187A0FFC
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PIR; F98026; F98026.

GO; GO:0004556; F:Alpha-amylase activity; IEA.

GO; GO:0016798; F:hydrolase activity, acting on

GO; GO:0016798; F:carbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006589; Alpha_amyl_cat.

InterPro; IPR006589; Alpha_amylase; 1.

Pfam; PF00128; alpha-amylase; 1.
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AKSGLAALITDGPGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSI
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                                                                                                        QVFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSA
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                                                                        CVFYGDYYGISGQYAQQ--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN-
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3 (TrEMBLrel. 23,
3 (TrEMBLrel. 24,
3 (EC 3.2.1.1).
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nicutes; Lactobacillales; Streptoco
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p06278 bacillus am
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p26613 salmomella
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p19531 bacillus sc
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## ALIGNMENTS

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SEQUENCE OF 1-29 FROM N.A. SEQUENCE OF 1-29 FROM N.A. MEDLINE=89213924; PubMed=2540150; MEDLINE=89213924; PubMed=2540150; Laoide B.M., Chambliss G.H., McConnell D.J.; Tacillus licheniformis alpha-amylase gene, amyL, is subject to promoter independent catabolite repression in Bacillus subtilis."; J. Bacteriol. 171:2435-2442(1989). [6] [6] [7] MEDLINE=82098050; PubMed=6172418; Kuhn H., Fietzek P.F., Lampen J.O.; Kuhn H., Fietzek P.F., Lampen J.O.; Kuhn H., Tetrainal amino acid sequence of Bacillus licheniformis	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Requadt C.; "Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus and Bacillus licheniformis."; J. Bacteriol. 166:635-643(1986).  [3] SECUENCE FROM N.A. Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaei A.A.; Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaei A.A.; "An unusual DNA sequence encoded a hyperthermostable alpha-amylase."; "Shahhoseini M. Siaei A.A., Ghaemi N., Pourbabaei A.A.; "An unusual DNA sequence encoded a hyperthermostable alpha-amylase."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  [4] "SUUENCE OF 1-104 FROM N.A. MEDLINE=8418545; PubMedd=6609154; Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; Stephens M.A., Ortlepp S.A., Ollington of the Bacillus licheniformis alpha-amylase gene: comparison with the B. amyloliquefaciens gene."; J. Bacteriol. 158:369-372(1984).	SEQUENCE FROM N.A.  STRAIN=ARCC 27811;  MEDLINE=86111694; PubMed=2418011;  YUUKİ T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,  YUUKİ T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Udaka S.;  Tsukagoshi N., Tsuboi A., Yamagata H.,  Tsuki T., Yamagata H.,  Tsukoi A., Yamagata H.,  Tsukoi	HACLI STANDARD; PRT; 512 AA.  AMY BACLI STANDARD; PRT; 512 AA.  POGZZE. OB4IZL; 01-JAN-1988 (Rel. 06, Created) 01-JAN-1988 (Rel. 06, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (BLA).  AMYS OR AMYL.  Bacillus licheniformis. Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.  NCBI TaxID=1402;

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STRAIN-ATCC 27811;
MEDIINE-ST82462; PubMed=7877175;
Machius M., Wiegand G., Huber R.;
"Crystal structure of calcium-depleted Ba"
amylase at 2.2-A resolution,"
T Mol. Biol. 246:545-559(1995).
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MUTAGENESIS OF ASP.
ASN-217; ASN-219; /
AND GLU-365.
STRAIN-ATCC 6598;
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J. Mol. Biol. 301:1041-1057(2000).

[11]

MUTAGENESIS OF GLN-293 AND ASN-294.

STRAIN=ATCC 6598;

WEDLINE=22622102; PubMed=12736372;

MEDLINE=22622102; PubMed=12736372;
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MEDLINE=21992788; PubMed=11997021;.
Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
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TEBS Lett. 518:79-82(2002).
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J. Bacteriol. 149:372-373(1982).
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STRAITA-ATCC 6598;

MEDLINE=96367070; PubMed=8771184;

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multiple amino acid replacements and molecular modelling.";

Protein Eng. 8:1029-1037(1995).
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                          disorder-->order transition
by a calcium-sodium-calcium
Structure 6:281-292(1998).
                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLLNE=98212915; PubMed=9551551;
MEDLLNE=98212915; PubMed=9551551;
MAChius M., Declerck N., Huber R., Wiegand G.;
"Activation of Bacillus licheniformis alpha-amylase through disorder--order transition of the substrate-binding site me by a calcium-sodium-calcium metal triad.";
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STRAIN=ATCC 27811;
MEDLINE=22797417; PubMed=12915728;
Rivera M.H., Lopez-Munguia A., Soberon X.,
"Alpha-amylase from Bacillus licheniformis
catalytic site: effects on hydrolytic and t
                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                                                                                                                                                               Protein
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19; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300;
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C STRAIN-ATCC 6598;

X MEDIINE-22538505; PubMed=12540849;

A Machius M., Declerck N., Huber R., Wiegand G.;

Machius M., Declerck N., Huber R., Wiegand G.;

Machius M., Declerck N., Huber R., Wiegand G.;

Machius M., Declerck N., Huber R., Wiegand G.;

Machius M., Declerck N., Huber R., Wiegand G.;

Mixinetic stabilization of Bacillus licheniformis alpha-amylase thrule introduction of hydrophobic residues at the surface.";

J. Biol. Chem. 278:11546-11553(2003).

J. Biol. Chem. 278:11546-11553(2003).

J. Biol. ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

C. Inkages in oligosaccharides and polysaccharides.

C. Inkages in oligosaccharides and polysaccharides.

C. Introduction of sinds 3 calcium ions and 1 sodium ion per subunit.

C. Introduction of starch-containing mashes and in the detergent industry to remove starch. Sold under the name Termamyl by
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Svendsen A., Borchert T.V., Dauter
"Structural analysis of a chimeric
High-resolution analysis of native
Biochemistry 39:9099-9107(2000).
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H162V/N219F/A238V/Q293S/N294Y.
STRAIN-ATCC 6598;
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MISCELLANEOUS: Able to work at relatively high
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BL; M38570; AAA22240.1; -.
BL; M13256; AAA22240.1; -.
BL; K01984; AAA22240.1; -.
BL; K01984; AAA22193.1; -.
BL; AF438149; AAA2237.1; -.
BL; AF438149; AAA2237.1; -.
BL; A1930; CAA01355.1; -.
BL; A1997; ALBSL.
B; 1BLI; 23-MAR-99.
B; 1BFL; 17-AUG-96.
B; 1BSL; 17-AUG-96.
B; 1BSL; 21-UN-01.
B; 1E3Z; 24-UN-03.
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01-JAN-1988
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Kaeaeriaeinen L.;
"Amino acid sequence of alpha-amylase deduced from the nucleotide sequence c J. Biol. Chem. 258:1007-1013(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucanohydrolase).
Bacillus amyloliquefaciens.
Bacteria; Firmicutes; Bacil
NCBI_TaxiD=1390;
                                                                                                                SEQUENCE OF 32-222,
MEDLINE-80241725; PubMed-6156671;
Chung H.S., Friedberg F.;
"Sequence of the N-terminal half."
                                                                                                                                                                                                                                                                                                                                           MEDLINE=83108808; PubMed=6185474;
Takkinen K., Pettersson R.F., Kalkkinen
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     EMBL; J01542; AAA22191.1; -.
EMBL; V00092; CAA23430.1; -.
EMBL; A20154; CAA01489 1; -.
EMBL; M18424; AAA22192.1; -.
PIR; A92389; ALBSN.
PDB; 1E3X; 21-JUN-01.
PDB; 1E3X; 22-JUN-03.
PDB; 1E40; 24-JUN-03.
PDB; 1E43; 21-JUN-01.
InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006048; Alpha_MYLASE.
PFam; PF00128; Alpha-amyla8e; 1.
PFam; PF00128; Alpha-amyla8e; 1.
PRNINTS; RM00642; Aamy; 1.
Carbohydrate metabolism; Hydrola8e; Gly
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MEDLINE-88137952; PubMed-2830166;
Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase its own signal peptide from Saccharomyces cerevisiae host cells."
Gene 59:161-170(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-20384196; PubMed=10924103;
Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen Brzozowski A.M., Lawson D.M., Turkenburg J.P., Busgaard-Frantzen Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
Structural analysis of a chimeric bacterial alpha-amylase.
High-resolution analysis of native and ligand complexes.";
Biochemistry 39:9099-9107(2000)
-1- CAPALYFIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-1- COPACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
-1- SUBURIT: Monomer.
-1- SUBURIT: Monomer.
-1- SUBURIT: Belongs to family 13 of glycosyl hydrolases.
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Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M., Soederlund H., Takkinen K., Kaeaeriaeinen L.; "Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens."; Gene 15:43-51(1981).

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Hydrolase; Glycosidase; Calcium-binding;

M 1.

M 2 AND SODIUM.

M 2 (VIA CARBONYL OX)

M 1 AND SODIUM.

M 1 AND SODIUM.

M 1 AND SODIUM.

M 2.

M 2.

M 3 (VIA CARBONYL OX)

M 3 (BY SIMILARITY).

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JM 1 (IN REF. 2).

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SEQUENCE OF 1-96; FROM N.A. ; PubMed=6170539;

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Best Local Simi
Matches 388;
                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.

MEDINE-88162814; PubMed=3258152;

Tsukamoto A., Kinura K., Ishii Y., Takano T., Yamane K.;

Tsukamoto A., Kinura K., Ishii Y., Takano T., Yamane K.;

"Nucleotide sequence of the maltohexaose-producing amylase gene
an alkalophilic Bacillus sp. #707 and structural similarity to
liquefying type alpha-amylases ",

Biochem. Biophys. Res. Commun. 151:25-31(1988).

-!- CAPALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic lin
in amylaceous polysaccharides so as to remove successive
maltohexaose residues from the non-reducing chain ends.

-!- COPACTOR: Binds 2 calcium ions and 1 sodium ion per subunit
                                                                                                                                                                                                                                                                                                                                                                               Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98)
(Maltohexaose-producing amylase) (Exo-maltohexaohydrolase)
Bacillus sp. (strain 707)
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI TaxID=1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                              similarity).

PATHWAY: Starch degradation.

PATHWAY: Starch degradation.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to family 13
    SWISS-PROT
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Pred. No. 9
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PIR, A27705, A27705.

HSSP; P06278; 1VJS.

InterPro; IPR006589; Alp amyl_cat_sub.

InterPro; IPR006047; Alpha amyl_cat.

InterPro; IPR006046; Glyco_hydro_13.

Pfam; PF00128; alpha-amylase; 1.

PRINTS; PR00110; Alpha-amylase.

SMART; SM00642; Aamy; 1.

Hydrolase; Glycosidase; Carbohydrate met
SIGNAL

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                                                                  HPNSGLATIMSDGAGGSKWMFVGRNKAGQVWSDITGNRTGTVTINADGWGNPSVNGGSVS
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MEDLINE=86059211; PubMed=2999073; Tsukagoshi N., Iritani S., Sasaki T., Idota Y., Yamagata H., Udaka S.; "Efficient synthesis and secretion of protein-producing Bacillus brevis 47 c stearothermophilus amylase gene."; J. Bacteriol. 164:1182-1187(1985).
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                                                                                            MEDLINE=21125602; PubMed=11226887;
Suvd D., Pujimoto Z., Takase K., Matsumura M., Mizumo H.;
"Crystal structure of Bacillus stearothermophilus alpha-amylase:
possible factors determining the thermostability.";
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MEDLINE=86008166; PubMed=3876333;
Ihara H., Sasaki T., Tsuboi A., Y
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Bacteria; Firmicutes; Bacillales;
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EMBL; X02769; CAA26547.1; -.
EMBL; M57457; AAA22227.1; -.
EMBL; M13255; AAA22241.1; -.
PIR; A24436; A24436.
PIR; A91999; ALBSF.
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InterPro; IPR00646; Glyco_hydro_13.
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MCDLINE=21534948; PubMed=11677609;
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Enterobacteriaceae; Salmo
                                             Kawagishi I., Mueller V., Williams A.W., Irikura V.M., N
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J., Bacteriol. 174:6644-6652(1992).
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239
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J. Gen. Microbiol. 139:1401-1407(1993).
I. CARALTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic CARALTIC ACTIVITY: Endobydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
IINKAGES in oligosaccharides and polysaccharides.
ICOPACTOR: Binds 1 calcium ion per subunit (By similarity).
ISUBUNIT: Monomer (By similarity).
ISUBUNIT: Monomer (By similarity).
ISUBCELLULAR LOCATION: Cytoplasmic.
ISUBCELLULAR LOCATION: Cytoplasmic.
ISUBCELLULAR LOCATION: Cytoplasmic.
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InterPro; IPR006589; Alpha amyl.
InterPro; IPR006047; Alpha amy
Pfam; PF00128; alpha-amylase;
SMART; SM00642; Aamy; 1
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EMBL; ABC008787; AAL20875.1; -.
EMBL; M85241; AAA27079.1; -.
EMBL; L13280; AAA71970.1; -.
EMBL; L13280; AAA71970.1; -.
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Raha M., Kihara M., Kawagishi I., Macnab R.M.;
"Organization of the Escherichia coli and Salmc
chromosomes between flagellar regions IIIa and
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StyGene; SG100
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                                         GGGYDMRKLINGTVVSKHPIKSVTFVDNHDTQPGQSIESTVQTWFKPLAYAFILTRESGY
                                                                                                               SFLRDWVNHVREKTGKEMFTVÅEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHÄASTQ
                                                                                                                                                                             GKAWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKF
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                                                                                                WFYKEWIEHVQAVAPKPLFIVAEYWSHEVDKLQTYIDQVDGKTMLFDAPLQMKFHEASRQ
                                                                                                                                                       GDGWNDQVDDEMGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQTHCDGFRLDAVKHIPA
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llarity 42.4%;
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RESULT 6
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P26612; P780
01-AUG-1992
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Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., (Mau B., Shao Y.;
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01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizohuchi K., Mori H., Mori T., Motomur Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93015717; PubMed=1400215;
Raha M., Kawagishi I., Mueller V., Kihara
"Escherichia coli produces a cytoplasmic a
J. Bacteriol. 174:6644-6652(1992).
                                       STRALBUBLE: STRALBUBLE: PubMed=8371104;
MEDLINE=93381452; PubMed=8371104;
Raha M., Kihara M., Kawagishi I., Macnab R.M.;
"Organization of the Escherichia coli and Salmonella
"Organization of the Escherichia coli and Salmonella
"Organization of the Escherichia coli and IIIb,
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Itoh T., Aiba H.,
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                         MEDIINE=92407478; PubMed=1527488; Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Marawagishi I., Mueller V. Williams A.W., Irikura V.M., Marawagishi I., Mueller V., Williams A.W., Irikura V.M., Marawagishi I. Generichia of "Submonella typhimurium chromosomes and identification of additional flagellar genes.";

J. Gen. Microbiol. 138:1051-1065(1992).
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Goeden M.A., Rose D.J.,
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EMBL; AE000285; AAC74994.1; -.
EMBL; D90833; BAA15755.1; -.
EMBL; M85240; -; NOT ANNOTATED_CDS
EMBL; L13279; AAA82575.1; -.
EDR; D64956; A45738.
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                                                             TQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRES
                                                                                                                                                 YTGEGWNDQVDDELGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQTQCDGFRLDAVKHI
                                                                                                                                                                       FQGKAWDWEYSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHI
                                                                                                                                                                                                DDRTQI--DEBIIECEGWTRYTFPARAGQYSQFIWDFKCFSGIDHIENPDEDGIFKIVND
                                                                                                                                                                                                                        ADRNRVISGEHLI--KAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYK----
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                         GYPQVFYGDMYGTK----
                                                                                                 PAWFYKEWIEHVQEVAPKPLFIVAEYWSHEVDKLQTYIDQVEGKTMLFDAPLQMKFHEAS
                                                                                                                      KFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNENHSVFDVPLHYQFHAAS
GVPSVFYPDLYGAHYEDVGGDGQTYPIDMPIIE-QLDELILARQRFAHGVQTLFFDHPNC
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Alpha-amylase (EC 3.2.1.1)]
Paenibacillus polymyxa (Bacillus polymyxa)
Bacteria; Firmicutes; Bacillales; Paenibacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A single gene directs synthesis of a proand alpha-amylase activities in Bacillus J. Bacteriol. 171:375-382(1989).
            This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                                                                                                                                                                     Rhodes C., Strasser J., Friedberg F.;
"Sequence of an active fragment of B.
Nucleic Acids Res. 15:3934-3934(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-776 FROM N.A. STRAIN=ATCC 8523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89123046; PubMed-2464578;
Uozumi N., Sakurai K., Sasaki T.,
Tsukagoshi N., Udaka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsukagoshi N., Udaka S.;
"Cloning and nucleotide sequence of the geactive fragments of the Bacillus polymyxa g. Bacteriol. 169:1564-1570(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawazu I.,
Tsukagoshi
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Kawazu T., Nakanishi Y., Uozumi N.,
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                                                                                                                                                                                                                                                                   Biochemistry 30:4594-4599(1991).
-!- FUNCTION: THE PRECURSOR PROTEIN PRODUCE MULTIFORM BETA-AMYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87231094; PubMed=2438660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1406;
                                                                                                                                                                                                                                                                                                               polymyxa beta-amylase
                                                                                                                                                                                                                                                                                                                             MEDLINE=91215008; PubMed=1827035;
Uozumi N., Matsuda T., Tsukagoshi
"Structural and functional roles
                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BOND,
                                                                                                                polysaccharides so as to remove successive maltose non-reducing ends of the chains.

CATTALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-gl linkages in oligosaccharides and polysaccharides. SUBCELLULAR LOCATION: Secreted.

SUBJULTARITY: In the N-terminal section; belongs to glycosyl hydrolases.

SIMILARITY: In the C-terminal section; belongs to SIMILARITY: In the C-terminal section;
                                                                                                                                                                                                                   SECRETION.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in nolvsaccharides so as to remove successive maltose units from the
                                                                                                    glycosyl hydrolases.
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onal roles of cysteine residues
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                                                                                                                                                   section; belongs to family 14
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                                                                                                                                                                             is of 1,4-alpha-glucosidic polysaccharides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor protein with beta-
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D A 48 kDa ALPHA-AMYLASE
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xa beta-amylase.";
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pfam; pF02806; alpha-amylase C; 1.
pfam; pF03423; GBM 25; 2.
pfam; pF03423; GBM 25; 2.
pfam; pF01373; GlyCo_hydro_14; 1.
pRINTS; pR00110; ALPHAAMYLASE.
pRINTS; pR00750; BETAAMYLASE.
pRART; SM00642; Aamy; 1.
sMART; SM00642; Aamy; 1.
sMART; SM00632; Aamy; 1.
pR0SITE, pS00506; BETA_AMYLASE_1; 1.
pR0SITE, pS00679; BETA_AMYLASE_2; 1.
pR0SITE, pS00679; BETA_AMYLASE_2; 1.
pR0SITE, pS00679; BETA_MYLASE_2; 1.
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EMBL; Y00150; CAA6834
PIR; A29130; A29130.
HSSP; P36924; 1B9Z.
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InterPro; IPR001554; Glyco_hydro_14.
Pfam; PF00128; alpha-amylase; 1.
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InterPro; IPR006047;
InterPro; IPR005085;
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NGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFŚFLRDWVNHVR
                                                                                                                                                                                                                  GTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVIS
                                                                                                          GEHLIKAWTHFHFPGRGSTYSDF-KWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNE
                                                                                                                                                                 -AVDGHLGTMDKLQELVRKAHDKNÍAVMVDVVVNHTGDFQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA85446.1;
CAA68344.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degradation; Repeat.
                                                                                                                                                                                                                                                                         -ĠGDFQGIINKLDYIKOMĠFTAIWİTPVTMQKŚEYAYHĠYHTYDFY------
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Alpha_amyl_c.
Alpha_amyl_cat.
CBM_25.
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                                                            PGNGFAKAPFDKADWYHINGDI TDGDYNSNN
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BY SIMILARITY.
C-SS: 5-FOLD DECREASE IN ACTIVITY.
C-SV: 20-FOLD DECREASE IN ACTIVITY.
C-SG: 60-FOLD DECREASE IN ACTIVITY.
M -> MIGL (IN REF. 3).
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BETA-AMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                    Score 340; DB 1;
Pred. No. 4.2e-17;
1; Mismatches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-AMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A41EA6B70F257064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosidase; Signal;
                                                                                                                                                                                                                                                                                                                                                                                         175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Indels 158;
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                                                            ----QWKI--E
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                                                                                                                                                                             865
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                                                                                                                         189
                                                                     901
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RESULT 8
AMYA_VIGMU
ID _AMYA_V
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94120017; PubMed-8290640;
Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
"Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
Plant Physiol. 103:1459-1459(1993).

-!- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CAPACTOR: Binds 3 calcium ions per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBUNIT: Monomer (By similarity) 13 of glycosyl hydrolases.
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; X53049; CAA37217.1; -.
EMBL; X73301; CAA51734.1; -.
FIR; S10514; S10514.
HSSP; P04063; 1AVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamauchi D., Minamikawa T.;
"Nucleotide sequence of cDNA for alpha-amylase from cotyledons germinating Vigna mungo seeds";
Nucleic Acids Res. 18:4250-4250(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cotyledon;
MEDLINE=90332425; PubMed=2377468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vigna mungo (Rice bean) (Black gram).

Pukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (BC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMYA_VIGMU
P17859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYSDDRYYRDAQTNGVFIDNHDVK--RFLNDASGKPGANYDKWPQL---KAALGFTLT-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSSVANSGLAALITDGPGGAKKMYVGRQNAGETWHD-----ITGNRSEPVVINSEGW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGIPIIYQGTEQGYSGGDD---PA-----NRENMNFNANHDLYQYIAKLNYVRNN 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKTGKEMFTVAEYWQNDLGALENYLNKTNENHSVFDVPLHYQFHAASTQGGGYDMRKL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DQAANTFIMGEIFHGDPAYVGDY---TRYLDAALDFPMYYTI--KDVFGHDQSMRKIKD 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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IPR006589; Alp\_amyl\_cat\_sub IPR006047; Alpha\_amyl\_cat.

date da da o o o o

glucan glucanohydrolase). AMY1.2 OR AMY3A.

on update) (EC 3.2.1.1)

(1,4-alpha-D

8

Oryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

RESULT AM3A\_OR

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Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAPMYLASE.
SMART; SM00642; Aamy; 1.
Carbohydrate metabolism; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  POCAT
                                                                                                        259
                                                                                                                                   279
                                                                                                                                                             204
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                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                       122
359 SIR-----LRNGINEKSTVKIMASEGDLYVAKIDNKIMVKIGP 396
                          389 KARKQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGP 432
                                                                                                                                                                                                                                                                                                127 RVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGT-----DWDESRKLNRIYKFQGKA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                   126;
                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                               26 LFQGFNWESSKKGGWYNSLKNSIPDLANAGITHVWLPPPSQSVSPE--GYLPGRLYDLD-
                                                                                                                                                                                                                                                                                                                                                                                                        7 LMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                          SLESTVQTWFKP----LAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPIL
                                                                                                                                                                                                                                          W----DWEVSNENGNYD----YLMYADIDYDHPDVAAEIKRWGTWYANELOLDGFRLDAV 233
                                                   --GSTQRLWPFPSDKVMQGYAYILT-HPGTPSIFYDHFFDW------
                                                                                                       GAITAFDFTTKGILQAA-VQG---ELWRLIDPNGKPPGMIGVKPENAVTFIDNHDT----
                                                                                                                                 FWHSVFDVPLHYQFHAASTQGGGYDMRKLL--NGT---VVSKHPLKSVTFVDNHDTQPGQ 333
                                                                                                                                                                                      KHIKFSFLRDWVNHVREKTGKEMFTVAEYW-------QNDLGALENYLNKTN 278
                                                                                                                                                                                                                FICRDDTAYSDGTGNNDSGEGYDAAPDIDHLNPQVQRELSEWWNWLKTEIGFDGWRFDFV
                                                                                                                                                                                                                                                                                                                                                   FHOKGTVRTKYGTKGELOSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRN 126
                                                                                                                                                             KGYAPSISKIYM----EQT-KPDFAVGEKWDSISYGQDGKPNYNQDSHRGALVNWVESAG
                                                                                                                                                                                                                                                                                                                            -----ASKYGSKNELKSLIAAFHEKGIKCLADIVINHR----TAERKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
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                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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BY SIMILARITY.

CALCIUM 1 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).

CALCIUM 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 311.5;
Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .4e-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 131;
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                                                    -GLKEQIAKLS
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InterPro, IPRO06047; Alpha amyl cat.
InterPro, IPRO06046; Glyco hydro 13.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X56336; CAA39776.1;
PIR; S14958; S14958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CINKAGES in oligosaccharides and polysaccharides.
CORACTOR: Binds 3 calcium ions per subunit (By similarity).
SUBUNIT: Monomer.
TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
DEVELOPMENTAL STAGE: Expressed at a high level during germination
in the aleurones cells under the control of the plant hormone
gibberellic acid and in the developing grains at a low level.
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      germination.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
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                                      126
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vdrate metabolism;
                                                                             89
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                                      NRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDG-----TDWDESRKLNRIYKFQGK
                                                                                                                   EFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADR
                                                                                                                                                            LFQGFNWDSWKKQGGWYNMLKDQVGDIÄSAGVTHVWLPPPTHSVSPQ--GYMPGRLYDLN
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440
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207
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166
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  -DGRG-VYCIFK---
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AM3C OR
P27939;
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Sutliff T.D., Huang N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alpha-amylase isozyme 3C precursor (EC 3.2.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sutliff T.D., Huang N., Litts J.C., Ro "Characterization of an alpha-amylase Plant Mol. Biol. 16:579-591(1991).
               PIR; $14956; $14956.

HSSP; $04063; IAVA.

Gramente; $P27939; ...

InterPro; IPR006589; Alp amyl_cat_sub.

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006046; Glyco_hydro_cat.

InterPro; IPR006046; Glyco_hydro_cat.

Pfam; $P500128; alpha_amylase; 1.
                                                                                                                                                         modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                              EMBL; X56338; CAA39778.1;
PIR; S14956; S14956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                   SUBUNIT: Monomer.

TISSUE SPECIFICITY: Germinating seeds.

TISSUE SPECIFICITY: Germinating seeds.

DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.

SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAFDFTTKGILQSA-VQGELWRWRD-KDGKAPGMIGWYPEKAVTFVDNHDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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se multigene cluster in
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                                                                                                                                                                             moved. Usage by and for (See http://www.isb-sib.
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Pfam; Pr PRINTS;

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Carbohydrate
Signal; Multi
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METAL 1

Query Match Best Local

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_BACS8 STANDARD; PRT; 713 AA.
CLOT_BACS8 STANDARD; PRT; 713 AA.
P17692;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclomalicdextrin glucamotransferase precursor (EC 2.4.1.19)
Cyclomalicdextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
amylase).
Bacillus sp. (strain B1018)
Bacteria; Firmicutes; Bacil
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ydrate metabolism; Hydrolase;
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                                                                                                                                                                                                                                                                        RKQ 393
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437
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BY SIMILARITY
BY SIMILARITY
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Pred. No. le-14;
8; Mismatches 1
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             Bacillaceae;
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Matches 113
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InterPro; IPR002909; IPT TIG.
Pfam; PF00128; alpha-amylase; 1
Pfam; PF00128; alpha-amylase_C;
Pfam; PF00183; TIG; 1.
Pfam; PF0183; TIG; 1.
Pfam; PF00110; ALPHAAMYLASE.
PRINTS; PR00110; ALPHAAMYLASE.
PRODOM; PD001560; CBD_4; 1.
SMART; SM00642; Aamy_C; 1.
SMART; SM00632; Aamy_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as not sembodified and this statement is not removed. Usentities requires a license agreement (See htt or send an email to license@sisb-sib.ch).
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ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       digest raw starch.
-[- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
-[- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
-[- SUBCELLULAR LOCATION: Secreted.
-[- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M33302; AAA22239.1; --
EMBL; D90112; BAA14140.1; --
PIR; S09196; S09196.
HSSP; P43379; 1CDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucanotransferase genes.";
Biochem. Biophys. Res. Commun.
-!- FUNCTION: This endo-type a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Itkor P., Tsukagoshi N., Udaka S.;
"Nucleotide sequence of the raw-starch-digesting amylase gene Bacillus sp. B1018 and its strong homology to the cyclodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1417;
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SIGNAL
                                                                                                                                                                          SEQUENCE
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                                                78
                                                                             19
                                                                                                            al Similarity
113; Conserv
                 73
               VRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGE
                                                                        GQHWRRLQN--DSAYLAEHGITAVWIPP----AYKGTSQADVGYGAYDLYDLGEFHQKGT
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IPRO06048; Alpha_amyl_c.
IPRO06047; Alpha_amyl_cat.
IPRO02044; CBD_4.
IPRO06046; GBJYCo_hydro_13.
                                                GGDWQGIINKINDGYLTGMGVTAIWISQPVENIYSIINYSGVNNTAYHGYWARDFKK---
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IPR002909; IPT TIG.
0128; alpha-amylase; 1.
2806; alpha-amylase_C;
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                                                                                                             Conservative
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217
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23.8%;
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B6; Mismatches
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dsorbable amylase
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RESULT CDGT\_BA

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CDGT_BACSO STANDARD; PRT; 713 AA. P05618; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Cyclomaltodextrin glucanotransferas precurso cyclomaltodextrin glucanotransferas precurso (Company)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-87308036; PubMed=2957361;

MEDLINE-87308036; PubMed=2957361;

Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;

"Nucleotide sequence of the beta-cyclodextrin glucanotransferase
"Nucleotide sequence of the beta-cyclodextrin glucanotransferase
of alkalophilic Bacillus sp. strain 1011 and similarity of its am
acid sequence to those of alpha-amylases.";

J. Bacteriol. 169:4399-4402(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp. (burnicutes;
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
"X-ray structure of cyclodextrin glucanotransferase from alkalophilic Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBI_TaxID=1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yclodextrin-glycosyltransferase)
                                                                                                                                        CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.

COFACTOR: Binds 2 calcium ions per subunit.

SUBUNIT: Monomer.

MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE ANINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALIFOLIGOSACCHARIDE PRODUCED.

SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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     InterPro; IPR006589; Alp_amyl_cat_
InterPro; IPR006048; Alpha_amyl_cat_
InterPro; IPR006047; Alpha_amyl_cat_
InterPro; IPR006047; CBD_4.

InterPro; IPR002044; CBD_4.

InterPro; IPR006046; Glyco hydro_1
InterPro; IPR007110; IPTIG.
InterPro; IPR002909; IPT_TIG.
Pfam; PF00128; alpha-amylase_C; 1.
Pfam; PF00686; CBM_20; 1.
Pfam; PF00683; TIG; 1.
Pfam; PF00683; TIG; 1.
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PTCDOM; PD001568; CBD 4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
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     ; Alp_amyl_cat_sub.; Alpha_amyl_C.; Alpha_amyl_cat.; CBD_4.; Glyco_hydro_13.; Ig_1ike.;
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RESULT 12 CDGT\_BACSO

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RESULT 13
AMY3 WHEAT STANDARD; PRT; 413 AA.

ID AMY3 WHEAT STANDARD; PRT; 413 AA.

AC P0817;
D1-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan DE glucanohydrolase).

GN AMY1.1 OR ALPHA-AMY3.

OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooide
OC Triticeae; Triticum.

OX NCBI TaxID=4565;
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les 127; Conservative 8
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                                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooideae;
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; Pred. No. 5.2e-14;
89; Mismatches 173
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STRAIN-CV. Chinese Spring;
STRAIN-CV. Chinese Spring;
Baulcombe D.C., Huttly A.K., 1
Baulcombe D.C., Huttly A.K., 1
Jarvis M.G.;
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InterPro; IPR006047; Alpha_amyl_
InterPro; IPR006046; Glyco_hydro;
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; AlphaAMYLASE,
SMART; SM00642; Aamy; 1.
Germination; Carbohydrate metabo
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EMBL; M16991; AAA34259.1; -.
PIR; S0637; ALWI3
HSSP; P04063; LAVA
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l. Gen. Genet. 209:33-40(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. COPACTOR: Binds 3 calcium ions per subunit (By similarity). SUBUNIT: Monomer (By similarity).

SUBUNIT: Monomer (By similarity).

BYVELOPMENTAL STAGE: Expressed at a high level during germi in the aleurones cells under the control of the plant hormoglibberellic acid and in the developing grains at a low level similarity: Belongs to family 13 of glycosyl hydrolases.
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413
  -DTKYSNGRGHRDTGGGFDAAPDIDHLNPRVQRELSAWLNWLKTDLGFDGWRLDFAKGY
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llarity 25.7%;
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                          -YLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHI
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Pred. No. 3.4e-14;
6; Mismatches 155;
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01-JUL-1993 (Rel. 2
10-OCT-2003 (Rel. 4
Cyclomaltodextrin 9
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BACCI
CDGT_
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Nitschke L., Heeger K., Bender H., Schulz G.E.;
"Molecular cloning, mucleotide sequence and expression of the beta-cyclodextrin glycosyltransferase circulans strain no. 8.";
Appl. Microbiol. Biotechnol. 33:542-546(1990).
Parsiegla G., Schmidt A.K., Schulz G.E.;
"Substrate binding to a cyclodextrin glycosyltransferase mutations increasing the gamma-cyclodextrin production.";
Eur. J. Biochem, 255:710-717(1998).
-I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins of a 1,4-alpha-D-glucosidic bond.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus circulans.
Bacteria; Firmicutes;
                                                                                                                      MEDIINE=98226626; PubMed=9558324; Schmidt A.K., Cottaz S., Driguez H., Schulz G.E.; Structure of cyclodextrin glycosyltransferase complexed derivative of its main product beta-cyclodextrin."; Biochemistry 37:5909-5915(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30920;
                                                                                                                                                                                                                      MEDIINE=90064533; PubMed=2531228;
Hofmann B.E., Bender H., Schulz G.E.;
Hofmann B.E., Bender H., Schulz G.E.;
"Three-dimensional structure of cyclodextrin
Bacillus circulans at 3.4-A resolution.";
J., Mol. Biol. 209:793-800(1989).
                                                                                                                                                                                                                                                                                                                                   "Structure of resolution.";
                                                                                                                                                                                                                                                                                                                                                            Klein C.,
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InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006044; CBD 4.
InterPro; IPR006046; GlyGo hydro_13.
InterPro; IPR007010; Ig-11ke.
InterPro; IPR007010; Ig-11ke.
InterPro; IPR007010; ITT TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00128; alpha-amylase_C; 1.
Pfam; PF02806; alpha-amylase_C; 1.
Pfam; PF02806; alpha-amylase_C; 1.
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PRINTS; PR00110; Alpha-Amylase_Dr0Dom; PD001568; CBD_4; 1.
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PIR; S23674; ALBSGC.
PDB; 1CGT; 31-JAN-94.
PDB; 1CGU; 31-JAN-94.
PDB; 3CGT; 27-MAY-98.
PDB; 4CGT; 12-AUG-98.
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DB; 3CGT;
DB; 3CGT;
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DB; 7CGT;
DB; 7CGT;
DB; 9CGT;
InterPro;
InterPro;
InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001568; CBD
SMART; SM00642; Aamy;
SMART; SM00632; Aamy_(
                                                                                                                                                                                                                                                                                                                                        Transferase; (
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SUBUNIT: Monomer.

MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to family 13 of glycosyl hydrolases
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31-JAN-94.
31-JAN-98.
27-MAY-98.
12-AUG-98.
11-CCT-98.
 Glycosyltransferase; Calcium-binding; Signal;
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Best Local
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10-OCT-2003
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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclomaltodextrin glucanotransferase precurso
                                                                                                                                                                                                                                                                                                                                                        Bacillus sp. (strain (Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29335;
                                                                                                                                                                                                                                                                                                                                                                                                      (Cyclodextrin-glycosyltransferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOHWRRLON--DSAYLAEHGITAVWIPPA-----YKG-TSQADVGYGAYDLYDLGE
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rmicutes; Bacillales;
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Pred. No. 7.3e-14;
82; Mismatches 163
                                                                                                                                                                                                                                                                                                                                                           Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                        e precursor (CGTase).
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Best Local Similarity
Matches 118; Conserv
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Interpro; IPR006048; Alpha amyl_C.
Interpro; IPR006047; Alpha amyl_cat.
Interpro; IPR002044; CBD_4-
Interpro; IPR002044; CBD_4-
Interpro; IPR00710; Ig-1ike.
Interpro; IPR002909; IPT_TIG.
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Pfam; PF02018; alpha-amylase C; 1.
Pfam; PF0206; alpha-amylase C; 1.
Pfam; PF00686; CBM 20; 1.
Pfam; PF01833; TIG; 1.
PRINTS: PF0777
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ProDom; PD001568; CED_4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
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PIR; S21532; ALBSG6.
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or send an email to license@isb-sib.ch)
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          271
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          GWQKSWMSSI -- YVHKPVFTFGEWF---
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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# ALIGNMENTS

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A;Accession: A21663 A;Accession: A21663 A;Molecule type: DNA A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',85-67,'VA',70-71,'S',73-80,'D',8 A;Residues: 1-29,'LAO,'A;Residues: 1-29,	GB:W10346; WID:g14251 ree: NCIB 8061 ree: NCIB 8061 ree: NCIB 8061 89-372, 1984 sequence of the 5' ree A91796; MUID:84185455 A91796; MUID:84185453 STES GB:K01984; NID:g14243: GB:K01984; NID:g14243: and the 5'-end nucleot A21663; MUID:85076654	RESULT 1  ALBSL  ALBSL  Alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis [validated] - Bacillus l

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A;Note: sequence represents amino end of an internal fragment R;Machius, M.; Wiegand, G.; Huber, R. submitted to the Brookhaven Protein Data Bank, July 1995 A;Reference number: A65206; PDB:IBPL A;Contents: annotation; X-ray crystallography, 2.2 angstroms, A;Note: these structural studies suggest 163 is Leu rather tha R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W. submitted to the Brookhaven Protein Data Bank, October 1996 A;Reference number: A66860; PDB:IVJS
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J. Bacteriol. 149, 372-373, 1982
A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Machius, M.; Wiegand, G.; Huber, R.
J. Mol. Biol. 246, 545-559, 1995
A;Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase
A;Reference number: S53788, MUID:95182462; PMID:7877175
A;Accession: S53788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-29/Domain: signal sequence #status predicted <SIG>F;30-512/Product: alpha-amylase #status experimental <MAT>F;327-360/Domain: alpha-amylase core homology <a href="AWY">AWY">AWY">AWY">AWY</a>F;133,229,264/Binding site: calcium (Asn, Asp, His) #status ef;260,290,357/Active site: Asp, Glu, Asp #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; p
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A;Accession: 139772
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A; Residues: 30-37, 'E', 39-41, 'X', 43-47
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                    GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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C.Accession: A92389; Ayusu,, II.; Kalkkinen, N.; Falvo, ...
R.TTAKKinen, K.; Pettersson, R.F.; Kalkkinen, N.; Falvo, ...
J. Biol. Chem 258, 1007-1013, 1983
A.TITIE: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced from the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Relva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H. Gene 15, 43-51, 198
Gene 15, 43-51, 198
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
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A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
                                                                                                                                                                                     A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation A;Pathway: glycogen/starch degradation C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradat F;1-31/Domain: signal sequence #status predicted <SIG>F;1-31/Domain: signal sequence #status predicted <SIG>F;32-514/Product: alpha-amylase #status predicted <MPT>F;32-362/Domain: alpha-amylase core homology <AMY>F;133,331,266/Binding site: Calcium (Asn, Asp, His) #status predicted F;262,292,359/Active site: Asp) Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298 R;Rubbonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S. Gene 59, 161-170, 1987 A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells A;Reference number: 139763; MUID:88137952; PMID:2830166 A;Accession: 139763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Status: preliminary; translated A/Molecule type: DNA A/Residues: 1-39 <RE2>
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A; Residues: 1-96 < RES>
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Conservative
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                                                   (81.9%;
(80.3%;)
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Score 2184; D
Pred. No. 2.3e
44; Mismatches
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                                                   2.3e-147;
                                                                                                                 DB 1;
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                                                                                                      Length 514;
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VNGTLMQYFEWYTDNDGQHWKRLQNDAEHLSDIGITAVWIPDAYKGLSQSDNGYGPYDLY

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RESULT 3
A27705
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705
A;Accession: A27705
A;Roccule type: DNA
A;Residues: 1-518 <TSU>
A;Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g142497
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this org
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C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG-
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;34-518/Product: alpha-amylase core homology <AMY>
F;139,218,273/Binding slte: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted
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Matches
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LGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA
                                                                                          NGTLMQYFEWYMDNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD
                                                                    NGTMMQYFEWYLPNDGNHWNRLNSDASNLKSKGITAVWIPPAWKGASQNDVGYGAYDLYD
                                                                                                                                                  70.5%; llarity 67.8%; Conservative 6
                                                                                                                                               ; Score 1879; DB 1; Pred. No. 1e-125; 67; Mismatches 7
                                                                                                                                                                                         DB 1;
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A; Residues: 1-549 < JOR>
A; Residues: 1-549 < JOR>
A; Residues: 1-549 < JOR>
A; Cross-references: GB:X59476
A; Cross-references: GB:X59476
A; Experimental source: chromosomal DNA of strain DN1792
C; Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on to cycloment: Alpha-amylase genes have been found on plasmids and in multiple copies on to cycloment: Alpha-amylase genes have been found on plasmids and in multiple copies on to cycloment: Alpha-amylase of internal 1,4-alpha-D-glucosidic bonds
A; Start codon: GTG
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
A; Pathway: glycogen/starch degradation
C; Stepvords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polyse
C; Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polyse
F; 134/Domain: signal sequence #status predicted <MAT>
F; 139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F; 268,299,365/Active site: Asp, Glu, Asp #status predicted
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A;Title: Cloning of a chromosomal alpha-amylase gene A;Reference number: A54541
A;Accession: A54541
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                                                           LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 120
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                                 LYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEV
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LRDWVNHYREKTGKEMFTVAEYWONDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG
                                                                                                                                                                                                                                                                                            AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF
                                                                                                                                                                                                                                                                                                                             NRNOEVTGEYTIEAWTRFDFFGRGNTHSSFKWRWYHFDGVDWDQSRRLNNRIYKFRGHGK
                                                                                                                                NYDMRNIFNGTVVQRHPSHAVTFVDNHDSQPEEALESFVEEWFKPLAYALTLTREQGYPS
                                                                                                                                                GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
                                                                                                                                                                                              DRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKL-NRIYKPQ--GK 180
                                                                                      VFYGDMYG--TKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS
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                                                                 - VPAMRSKIDPILEARQKYAYGKQNDYLDHHNIIGWTREGNTA
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Bacillus stearothermophilus (strain DN1792)

#text \_change 13-Jun-1997

from Bacillus stearothermophilus.

8 the

polysacc

67.0%; 68; Score 1786.5; DB Pred. No. 4e-119; 8; Mismatches 9 DB 1; 98; Length 549; ເກ ~• Gaps 95 60

Asp

#status

predicted

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RESULT 5

A24549

A24549

A24549

A19ha-amylase (BC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)

A1pha-amylase (BC 3.2.1.1) precursor - Bacillus stearothermophilus

C; Dates: Bacillus stearothermophilus

C; Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999

C; Accession: A24549; I39501; I39770

R; Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.;

J. Bacteriol. 166, 635-643, 1986

A; Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus s

A; Reference number: A91817; MUID:86195857; PMID:3009417

A; Accession: A24549

A; PMID:3009417

A; Accession: A24549

A; Cross references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A; Cross references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A; Cross references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A; Cross references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A; Cross references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513

A; Accession: 170, 1034-1040, 1988

A; Fitle: Evidence for movement of the alpha-amylase gene into two phylogenetical

A; A; Cross references: GB:M25577; NID:g142476; PMID:3257753

A; Cross references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478

A; Cross references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478

A; Cross references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478

A; Cross references: GB:M25678; NID:G142484; DIN:AAA22225.1; DID:g142478

A; Cross references: GB:M25678; NID:G142484; DIN:AAA22225.1; DID:G142486

A; Cross references: GB:M25678; NID:G142484; DIN:AAA22225.1; DID:G142486

A; Cross references: GB:M25678; NID:G142484; DIN:AAA22225.1; DID:G142486

A; Cross references: GB:M25678; NID:G142484; DIN:AAA22225.1; DID:G142486

A; Cross referen
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation (;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology (;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; pt ;13-34/Domain: signal sequence #status predicted <SIG>F;13-34/Domain: alpha-amylase #status predicted <MAT>F;235-364/Domain: alpha-amylase core homology <AMY>F;139-327/Binding site: calcium (Asp, Asp, His) #status predicted
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A;Experimental source: strain 799
                                                                                                                                                                                        ;Start cod
;Function:
                                                                                                                                                                                                                                                        Comment: Alpha-amylase
                                                                                                                                                                                                              codon: GTG
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                                                                            C; Genetics:
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A; Residues: 1-45 < RES>
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                                                   A;Gene: amyS
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    me: plasmid
t codon: GTG
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121 DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQ--
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GGGYDMRKILNGTVVSKHPLKSYTFYDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGY
                                                                                                                                                                                                                                                                                             GKAWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKF
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                                                                        PCVFYGDYYGI---PQYNIPSIKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTE
                                                                                                           POVFYGDMYGTKGDSOREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS
                                                                                                                                              GGAFDMSTLMMNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGY
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Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plas
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence\_revision 18-Aug-1995 #text\_change 18-JunC;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1398
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Notecule type: DAAK
A;Residues: 1-549 <NAKS
A;Cross-references: GB:M11450
A;Cross-references: GB:M11450
A;Cross-references: GB:M11450
A;Note: amino end of the mature protein also determined
A;Note: amino end of the mature protein also determined
A;Note: amino end of the mature protein also determined
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A;Note: amino end of the mature protein also determined
A;Note: amino end of the mature protein also determined
A;Note: amino end of the mature protein also determined A;Title: In vivo genetic engineering: homologous recombination A;Reference number: I39772; MUID:91092499; PMID:2265757 A;Accession: I39777 A,Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; C,Comment: Alpha-amylase genes have been found on plasmids as A; Status: preliminary; translated from GB/EMBL/DDBJ l; PID:g142515 and in multiple g G 18-Jun-1999 ω plasmid tool for PAT5 copies plasmid

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C; Function: C; Function: C; Function: C; Function: C; Function: C; Supercription: C; Supercription: C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homolog C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homolog C; Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; F; 1-94/Domain: signal sequence #status predicted <SIG>F; 1-94/Product: alpha-amylase tatus experimental <MAT>F; 235-369/Domain: alpha-amylase core homology <AMY>F; 235-369/Domain: alpha-amylase core homology <AMY>F; 237, 272/Binding site: calcium (Asp, Asp; His) #status predicted F; 268, 298, 365/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase C;Species: Bacillus stearothermophilus C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 16-. C;Accession: A91999; B91999; A91804; A00845 R;Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; 1 J. Biochem. 98, 95-103, 1985 A;Reference number: A91999; MUID:86008166; PMID:3876333 A;Accession: A91999
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                                  A; Molecule type: protein
A; Residues: 35-48 <IH2>
                                                                              A; Molecule type: DNA
A; Residues: 1-548 <IH1
A; Residues: GB: X02769
A; Experimental source: plasmid
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Best Local
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Experimental source: strain DY-5;Tsukagoshi, N.; Iritani, S.; Sasaki,
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Pred. No. 2.1e-118;
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J. Bacteriol. 164, 1182-1187, 1985
A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase A;Reference number: A91804; MUID:86059211; PMID:2999073
A;Contents: pBAM101
A;Accession: A91804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation C;Superiamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core ho C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrol F;1-34/Domain: signal sequence #status predicted <SIG-F;35-548/Product: alpha-amylase #status experimental <MAT>F;235-368/Domain: alpha-amylase #status experimental <MAT>F;235-368/Domain: alpha-amylase core homology <AMY>F;239-327/272/Binding site: calcium (Asp. Asp. His) #status predicted F;268,298,365/Active site: Asp, Glu, Asp #status predicted
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A;Residues: 1-29,'Q',31-75,'W',77-122 <TSU>
C;Comment: Alpha-amylase genes have been found
C;Genetics:
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C;Function:
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Best Local Similarity
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                                                              NPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGI
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                                                                                                                                                                                                GGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTNPAKRC-SHGRPWFKPLAYAFTLTRQEGY
                                                                                                                                                                                                                       GGGYDMEKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGY
                                                                                                                                                                                                                                                                  SPPPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASKS
                                  IVVOR
                                                                                                                                                               POVFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS
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516
                                  483
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63.1%;
                                                                                                                                   - PQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1715; DB 1;
Pred. No. 4.8e-114;
7; Mismatches 106;
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4.8e-114;
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alpha-amylase (EC 3.2.1.1) - Bacillus circulans C;Species: Bacillus circulans C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1904 #sequence\_revision 10-Nov-1904 #sequence\_revision 10-Nov-1905 #sequence\_revision 10-Nov-1906 #sequence\_revision 10-Nov-1907 #sequence\_revision 10-Nov-

10-Nov-1995

#text\_change 22-Jun-1999

RESULT S15713

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alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
c/Species: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
c/pate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
c/Accession: AH2079
R;Kaneko, T.; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NA, Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy A;Accession: AH2079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 < KUR>
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A;Residues: I-493 <MAR>
A;Cross-references: EMBL:X60779; NID:g39411; PIDN:CAA43194.1; PID:g39412
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C;Superfamily: alpha-amylase, amyloliquefacters type; alpha-amylase core
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;200-333/Domain: alpha-amylase core homology <ANY>
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C;Function:
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Best Local Sim
Matches 230;
;Cross-references: GB:BA000019; pIDN:BAB73889.1; pID:g17131281; GSPDB:GN00179;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIY 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYGDYYGIGGPEPVDGKKEI-----LDILLSARCNKAYGEQEDYFDHANTIGWVRRGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYGDMYGTKG----DSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDLSKI FDDTLVQTHPTHAVT FVDNHDSQPHEALESWIGDWFKPSAYALTLLRRDGYPVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGTLMOYFEWYMPNDGOHWRRLONDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGEFDQKGTVRTKYGTKQELIEAIAECQKNGIAVYVDLVMNHKAGADETEVFKVIEVDPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHTMMQFFEWHLAADGDHWKRLAEMAPELKAKGIDTVWVPPVTKAVSAEDTGYGVYDLYD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.3%; Score 1262; DB 2; ilarity 47.6%; Pred. No. 5.9e-82; Conservative 75; Mismatches 166;
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alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
c/Species: Streptococcus pneumoniae
c/Species: Streptococcus pneumoniae
c/Accession: G95160
R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
on, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; FMID:11463916
A;Accession: G95160
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
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G95160
                                                                                                                                               A;Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-484 < KUR>
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                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                              SP1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 YPQVFYGDMYGTK-----GDSQRE---IPALKHKIEPILKARKQYAYGAQHDYFDHHDIV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 YPCVFHADYYGAEYEDWGKDGNRYNIFMPSHRWIIDKLLYARKHYAYGPQYNYLDHWNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 SGGNYDMRRILDGTMMQQRPTHAVTFVENHDSQPLQALESVVEPWFKPLAYAIILLRQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 QGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TWFFPEWIDALERHAGKDLFMVGEYWYNDINTLLWYVDAVRGXMSVFDVPLHYNFHQASK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 EGKNFDDYVALEKGNFAYLMGCDLDFQNEWVRGEVTYWGKWCLDTTKVDGFRIDAIKHIS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 QGKAWDWEVSNENGNYDYLMYADIDYDHPDVAABIKRWGTWYANELQLDGFRLDAVKHIK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 FSFLRDWVMHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 FPQDDRLNPKGGLQDIKTYTHYNFPGRQGKYSNFEWHWWHFDAVDYNEYNSGDRSTVYLL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 VDPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNR--IYKF 177
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47.5%; Pred. No. 1.1e~80;
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alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6) c.Species: Streptococcus pneumoniae (c.Species: C.Species:                                                                                                                                                                                                                                                                                                                    A;Gene: amy
C;Superfamily: alpha-amylase, amyloliquefaciens type;
C;Keywords: glycosidase; hydrolase
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                                                                                                                                                                                       NGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD
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                                   DRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQG--KA
                                                                                                                       LGEFHOKGTVRTKYGTKGELOSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPA
                                                                                                                                                               DRTVELGEPFTINGWTSFTFDGRQDTYNGFHWHWYHFTGTDYDAKRSKSGIYLIQGDNKG
                                                                                 Conservative
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                                                                                                                                                                                                                                                   Score 1228; DB 2;
Pred. No. 1.5e-79;
'5; Mismatches 166;
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                          YDMRKILNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                             DKWLEQRAKQLDRKLFIVGEYWSDDLGKLEYYLEQSSDRIQLFDVFLHFNMKEASSTNGE
                                                                                                                                                                                                         WDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFFRLDAVKHIKFSFL
                                                                                                                                                                                                                                                                                                                                       GEFDOKGTIPTKYGTKDEYLDLINTLHHNNIEVYADIVFNHMMGADETE---TIEADIKA
                                                                                                                                                                                                                                                                                                                                                                        GEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVD-PA 123
                                                                                                                                                                                                                                                                                                                                                                                                                       EDNHLHNIENNKTVEVWTKFTFPGRQGKYDNYIWTWHNFTGIDYDERKNQEBILEFEGHE
    FDMRTLFDHTLTASOPELSVTFVDNHDTOEGOALOSWIFAWFKEHAYSLILLRKKETPTV
                                                                                                                         RDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGGG
                                                                                                                                                                     WDENVDSENNNFDYLMGADLDFSVSETVEQLEKWGHWFSEMTKIDGFRLDAIKHIDFKYF
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420 -QSPIAVLISNDQENSKSMFVGQEWTNQTFVDLLGSHQGQVTIDEBGVGQFPVSARSVSV
                                                                                                                                                                                                                                                      GGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDWE--VSNENGNYDYLMYADIDYDHPDVAABIKRWGTWYANELQLDGFRLDAVKHIKFS
                                                                                                                                               QVFYGDMYGTKGDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSV
                                                                                                                                                                                                                            ANYDLRGIFTDSLVELKPDKAVTFVDNHDTQRGQALESTVEEWFKPAAYALILLRQDGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                          WANEELVDNENGNYDYLMYADLDFKHPEVIQNIYDWADWFMETTGVAGFRLDAVKHIDSF
                                                                                                                  CVFYGDYYGISGQYAQQ--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSGAEN-
                                                                                                                                                                                                                                                                                                                                   FMRNFIRDMKEKYGDDFYVFGEFWNSDKEANLDYLEKTEEHFDLVDVRLHQNLFEASQAG
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                                                            ANSGLAALITDGPGGAKKMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSI
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A;Status: <a href="LNA">A;Nolecule type: DNA</a>
A;Residues: 1-491 <STO>
A;Residues: 1-491 <STO>
A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1;
A;Cross-references: Strain IL1403 alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001
C;Accession: C86781 A/Experimental source: strain IL1403 C/Genetics: A/Gene: amyL C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: C86781 A;Status: preliminary R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, Genome Res. 11, 731-753, 2001 41.6%; Score 1108; DB 2; Length 491; 41.7%; Pred. No. 5e-71; tive 93; Mismatches 168; Indels 2 K.; Weissenbach, 24; GSPDB:GN00146 Lactococcus core homology Gaps lactis J.; Ehrli

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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98247
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A;Molecule type: DNA
A;Residues: 1-506 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Map position: linear chromosome;Superfamily: alpha-amylase;Superfamily: alpha-amylase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K----AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQG 179
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                                                                GEFHVNGGSVSIYV 481
                                                                                                               CIAFIRHGTADA---PGCVVVMSNGEPGEKQADLGPERÅGSVWRDFLGHREEHITLDESGK 487
                                                                                                                                                               IVGWTREGDSSVANSGLAALITDGPGGAKKNYVGRQNAGETWHDITGNRSEPVVINSEGW 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVE 119
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                                                                                                                                                                                                                EGVPCVFYPDLFGTSYTDTGNDGNEYKIDIPAIE-CLPKLIEARSRFANGPQTDIFDDAS 429
                                                                                                                                                                                                                                                                 SGYPQVFYGDMYGTK-----GDSQREIPALKHKIEPILKARKQYAYGAQHDYFDHHD 407
                                                                                                                                                                                                                                                                                                                 SKOGGDFDMRSIFDGSLVSAVPDHAVTLVDNHDTQPLQSLEAPVEPWFKPLAYAIILLRE
                                                                                                                                                                                                                                                                                                                                                                                                                IPAWFFRDWVGHMRETVDPDLFVVAEYWHPDLEALKSYLELVDKQLMLFDVALHHSFHDA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYGDGEWNEEVDQENGNFDYLMGADVEFRNRAVYEELKYWGRWLSEQVQVDGFRLDAAKH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNPDDRTDIDDEDFPALAYTRFTFPGRNGKHSKFIWDLKCFSGVDHIEEPTEDGIFRLVN 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKESELEDWYNHVEEKTGKEMETVAEYWQNDLGALENYLNKTNENHSVEDVELHYQFHAA 295
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Pred. No. 7.7e-70;
0; Mismatches 178; Indels 17;
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RESULT 15

#45738 alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Salmonella typhimurium
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A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
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C;Date: 11-Jan-2002 #text_change 18-Nov-2002
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608580; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
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AD3038
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                                                                                                                                                                                                                                        473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 RTDIDDEDFPALAYTRFTFPGRNGKHSKFIWDLKCFSGVDHIEEPTEDGIFRLVNEYGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 RNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGK---- 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQA-DVGYGAYDLYDL 64
                                                                                                                                                                                                                                      NGGSVSIYV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFDMRSIFDGSLVSAVPDHAVTLVDNHDTQPLQSLEAPVEPWFKPLAYAIILLREEGVPC
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                                                                                                                                                                                        NGGSVSVWV 490
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                                                                                                                                                                                                                                                                                                                                    REGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHV 472
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44.4%; Pred. No. 9.
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R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:93015717; PMID:1400215
A;Recession: B45738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation F;202-335/Domain: alpha-amylase core homology cAMY> F;239,265,332/Active site: His, Glu, Asp #status predicted
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A;Residues: 1-494 <RAH>
A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
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A;Gene: amyA
Function:
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;Accession: B45738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 208; Conservative
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                          239 SFLRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQ 298
480
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                                                                                                                                      411 WTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEF
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                                                                                                                                                                                                                                      359
                                                                                                                                                                                                                                                                               303 GAEYDMRHIFTGTLVEADÞFHAVTLVANHDTQÞLQALEAÞVEFWFKÞLAYALILLRENGV 362
                                                                                                                                                                                                                                                                                                                                    299
                                                                                                                                                                                                                                                                                                                                                                               243 WFYKEWIEHVQAVAPKPLFIVABYWSHEVDKLQTYIDQVDGKTMLFDAPLQMKFHEASRQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 39.8%; Score 1060; DB 1; Length 494; Similarity 42.4%; Pred. No. 1.3e-67; 08; Conservative 88; Mismatches 179; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKAMDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRTQIDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIENPDEDGIFKIVNDYT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYK----FQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLGEFDOKGTIATKYGDKROLLTAIDALKKNNIAVLLDVVVNHKMGADEKERIRVORVNO 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPTILQYFHWYYPDGGKLWSELAERADGLNDIGINWVWLPPACKGASGGYSVGYDTYDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGWNDQVDDEMGNFDYLMGENIDFRNHAVTEEIKYWARWVMEQTHCDGFRLDAVKHIPA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDP 122
FCNAGSVSVWV
                                             HVNGGSVSIYV 481
                                                                                                                                                                                      PSVFYPDLYGASYEDSGENGETCRVDMPVI-NQLDRLILARQRFAHGIQTLFFDHPNCIA
                                                                                                                                                                                                                                                                                                           GGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGY 358
                                                                                           FSRSGTEE - - NPGCVVVLSNGDDGEKTLLLGDNYANKTWRDFSGNRDEYVVTNDQGEATF
                                                                                                                                                                                                                                    PQVFYGDMYGT-----KGDSQR-EIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVG 410
490
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Search completed: May 3, 2004, 20:54:04 Job time : 14.7346 secs

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A;Note: sequence represents am no end of an internal fragment created by a single enz. R;Machius, M.; Wiegand, G.; Huber, R. submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A65206; PDB:1NFI
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210;222-511
A;Note: these structural studies suggest 163 is Leu rather than Arg
R;Song, H.K.; Hwang, K.Y.; Chang, S.W.
submitted to the Brookhaven Protein Data Bank, October 1996
A;Reference number: A6680; PDB:1VJS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference Number: 139772; MUID:91092499; PMID:2265757
A;Accession: V39772
A;Status: translated from GB/EMBL/DDBJ
A;Residues: Tabslated in GB/EMBL/DDBJ
A;Residues: Tabslated in GB/EMBL/DDBJ
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A;Title: In\vivo genetic engineering: homologous recombinati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Machius, M.; Wiegand, G.; Huber, R.
J. Mol. Biol. 246, 545-559, 1995
A;Title: Crystal structure of calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499
R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
J. Bacteriol. 149, 372-373, 1982
A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: A;Reference number; $26151; MUID:82098050; PMID:6172418
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A;Accession: S53788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein \A;Residues: 'D',220-227 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: prote
A;Residues: 30-37,'E',:
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A;Accession: A26151
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,30-51/Domain: alpha-amylase #status experiments
,227-360/Domain: alpha-amylase core homology <ANY,
,133,229,264/Binding site: calcium (Asn., Asp. His)
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Best Local (
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  330
                                              301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ 360
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                                                                                                                                                  LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQG
                                                                                                                                                                                                      AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKP
                                                                                                                                                                                                                                                 AWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELOLDGFRLDAVK
                                                                                                                                                                                                                                                                                                                                                      DPADRNRVISGEHLIKAWIHEHEPGRGSTYSDEKWHWYHEDGIDWDESRKLARIYKEQGK 180
                                                                                                                                                                                                                                                                                                                                                                                                      LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYDLGEFHOKGTVRTKYGTKGELOSAIKSLHSRDINVYGDVVINHKGKADATEDVTAVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANLNGTLMOYFEWYMPNDGOHWKRLONDSAYLAEHGITAVWIPPA
                                                                                                 LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANLNGTLMQYFEWYMPNDGOHWRRLQNDSAYLAEHGITAVWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalyzes the hydrolysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amyloliquefaciens type; alpha-amylase core homology tein; glycosidase; heat-stable protein; hydrolase; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2654; DB 1; \
Pred. No. 9.8e-181; \
2; Mismatches 1;
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TRESGYPO
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                                                       450 NSGLAALITDGPGGAKRMYVGRQNAGETWHDITGN
                                                                                                                                          361 VFYGDMYGTKGDSQREIPALKHKI
                                                                                   NSGLAALITDGPGGAKRMYVGRQNAGETWHD
                                                                                                                 VFYGDMYGTKGDSQREIPALKHKIEPID
                                                                                                                                       KPILKARKQYAYGAQHDYFDHHDLVGWTREGDSSVA 420
                                                                                                                 <u> АККОУАУСАОН БУГОННОТ</u>
                                                                             TGNRSEPVVINSEGWGEFHVNGGSVSIY 480
                                                       SEPVVINSEGWGEFHVNGGSVSIY
                                                         509
                                                                                                                  449
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alpha-effylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
\*\*Ffferrate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amyloliquefaciens
C;Species: Bacillus amyloliquefaciens
C;Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text\_change 18-Jun-1999
C;Accession: A92389; A90307; T39756; T39763; A00843
C;Accession: A92389; A90307; T39756; T39763; A00843
C;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; R;Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307 A;Molecule type: DNA A;Residues: 1-514 <TAK> A; Contents: pUB110 A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; A;Reference number: ;Accession: tie: Amino acid A92389 Palva, I.; Soderlund, H.; Kaariainen, PIDN: AAA22

A;Molecule type: protein A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU> R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, Gene 15, 43-51, 1981 A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region A;Reference number: I39756; MUID:82051296; PMID:6170539 Accession: I39756;

;Status: translated from GB/EMBL/DDBJ

;Residues: , Molecule type: DNA 1-96 <RES>

A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298 R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, & Gene 59, 161-170, 1987

Gene 59, 161-170, 1987 A;Title: Efficient secretion of Bacillus amyloliquefaciens A;Reference number: 139763; MUID:88137952; PMID:2830166 A;Accession: 139763 alpha-amylase cells by its

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-39 cRE2> A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431

A;Pathway: glycogen/starch degradation c;Superfamily: alpha-amylase core homology C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Reywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradate; F;1-31/Domain: signal sequence #status predicted <SIG> A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMYs
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status
F;262,292,359/Active site: Asp Clu, Asp #status predicted predicted

8 Matches 32 Similarity Conservative (81.9%; (80.3%;/ 44; Score 2184; DB 1; Pred. No. 2.3e-147; Mismatches Length 514; Indels ۲, Gaps 91 62

Q, ò

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RESULT 3
A27705
N)Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C; Species: Bacillus sp.
C; Dale: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C; Accession: A27705
R; Tsukanoto, A.; Kimura, K.; Ishii v. malano m
                                                                                                                                                                                                                                                                                                                                    A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradatics files alpha-amylase #status predicted cSIG>
F;1-33/Domain: signal sequence #status experimental <MAT>
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Qlu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-18 - 1873U>
A; Residues: 1-18 - 1873U>
A; Residues: 1-18 - 1875U>
A; Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g142497
A; Experimental source: chromosomal DNA of strain 707
A; Experimental source: chromosomal DNA of strain 707
A; Experimental source: chromosomal DNA of strain 707
A; Comment: This is the smallest of five starch-hydrolyzing enzymes from this cypunction:
C; Function:
A; Description: catalytes the hydrolysis of internal 1,4-alpha-D-glucosidic A; Pathway: glycogen/starch degradation
C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core how c; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation signal sequence #status predicted cSIG>
E; 1-33 Domain: signal sequence #status predicted cSIG>
E; 1-33 Domain: signal sequence #status predicted cSIG>
E; 1-35 Domain: signal sequence #status predicted cSIG>
E; 1-35 Domain: signal sequence #status predicted cSIG>
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A;Reference
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;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
iochem. Biophys. Res. Commun. 151, 25-31, 1988
;Title: Nucleotide sequence of the maltohexaose-producing amylase;Reference number: A27705; MUID:88162814; PMID:3258152
;Accession A27705
                                                                                                                                                                                                                                 Local Si
thes 329;
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                                                                                                                                                                                                                                                                      Similarity
      LGEFHQKGTVRTKYGTKGELQSAIKSLHSRD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQ
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                                                                                                  NGTMMQYFEWYLPNDGNHWNRLNSDASNLXSKGITAVWIPPAWKGASONDVGYGAYDLYD
                                                                                                                                               NGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQR 483
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                                                                                                                                                                                                                                                                   Score 1879;
Pred. No. 1
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                                                                                                                                                                                                                                                                   1e-125;
INVYGDVVINHKGGADATEDVTAVEVDPA
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                                                                                                                                                                                                                                                                                              Length
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A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core ho
C;Keywords: extracellular protein; dlycosidase; heat-stable protein; hydrol
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-549 <UOR>
A;Residues: 1-549 <UOR>
A;Cross-references: GB:X59476
A;Experimental source: chromosomal DNA of strain DN1792
C;Comment: Alpha-amylase genea have been found on plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B. FEMS Microbiol. Lett. 7, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene A;Reference number: A54341
A;Accession: A54541
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                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                Query Match
Best Local Sim
Matches 314;
                                                                                                                                                                                                                                                                         Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology, Keywords: extracellular protein, elycosidase, heat-stable protein, hydrolase, p. 1-34/Domain: signal sequence #status predicted <SIG>,35-549/Product: alpha-amylase #status predicted <MAT>
                                                                                                                                                                                                                                     ;35-549/Product: alpha-amylase #statbe predicted <MAT>;235-368/Domain: alpha-amylase core homology <AMY>;139,237,272/Binding site: calcium (Asp. Asp. His) #status
                                                                                                                                                                                                                       268,298,365/Active site: Asp, Glu, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514
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                                     61
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                                                                                                                                                                Similarity
HPNSGLATIMSDGAGGSKWMFVGRNKAGQVWSDITGNRTGTVTINADGWGNFSVNGGSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFYGDMYG--TKGDSQRETPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNENHSVEDVPLHYQFHAASTQGG
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                                                                           APFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLG
                                                                                                      ANLNGTLMQYFEWYMPNDGQHWRRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWDWEVDTENGNYDYLMYADIDMDHPEVVNÉLRNWGVWYTNTLGLDGFRIDAVKHIKYSF
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                                                                                                                                                  Conservative
                                                                                                                                                                67.0%;
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                                                                                                                                                  £83
                                                                                                                                                                Score 1788.5; DE
Pred. No. 4e-119;
                                                                                                                                              Mismatche
                                                                                                                                                                                                                     #status predicted
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"Sequence of
amylase.";
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MEDLINE=83108808; PubMed=6185474;
martinen K., Pettersson R.F., Kalkkinen N.,
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Bacillus amyloliquefaciens.
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Chung H.S., Friedberg F.;
"Sequence of the N-terminal
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X MEDLINE=20384196, PubMed=10924103,

BIZOZOWSKI A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,

X Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;

XI Structural analysis of a chimeric bacterial alpha-amylase.

YI High-resolution analysis of native and ligand complexes.";

High-resolution analysis of fative and ligand complexes.";

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MEDLINE=88137952; PubMed=2830166;

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Ruchonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;

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EMBL; V00092; CAA23430.1; -.
EMBL; A20154; CAA01489.1; -.
EMBL; A20154; CAA01489.1; -.
EMBL; M18424; AAA22192.1; -.
PIR; A92389; ALBSN.
PDB; 1232; 24-JUN-01.
PDB; 1232; 24-JUN-03.
PDB; 1243; 21-JUN-01.
InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006047; Alpha-amylase; 1.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAMYLASE.
SMART; SM00642; Aamy; 1.
Cataral, 20.54110110; Alpha-Mylase; Gl; 20.54110110; Alpha-Mylase; Gl; 20.54110110; Alpha-Mylase; Gl; 20.54110110; Alpha-Mylase; Gl; 20.54110110; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Gl; 20.5411010; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alpha-Mylase; Alp
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Matches 388;
                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.

WEDLINE-88162814, FubMed=>258152;

Teukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;

Teukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;

"Nucleotide sequence of the maltohexaose-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amylases.

1 in alpha-amylases. Pommun. 151.25-31(1988).

1-1 CARTALTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltohexaose residues from the non-reducing chain ends.

1-1 COPACTOR: Binds 2 calcium ions and 1 Sedium ion per subunit (By
                                                                                                                                                                                                                                                                                                                                       P1954;
P1954;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)
(Maltohexaose producing amylase) (Exo-maltohexaohydrolase).
Bactleria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                 -!- PATHWAY: Starch degradation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to family 13 of glycosyl
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80.3%; Pred. No. 9.8e-153;
tive 44; Mismatches 49;
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Interpro; IPRO06046; Glyco hydro 13.
Pfam; PRO0128; alpha amylase; 1.
PRINTS; PRO0110; ALPHAAMYLASE.
SMART; SMO6642; Aamy; 1.
Hydrolase; Glycosidase; Carbohydrate m
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PIR A27705; A27705.
HSSP P06278; IVJS.
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                                                             VANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGS
                                                                                            VFYGDYYGIPTHG-----VPAWRSKIDPILEARQKYAYGKQNDYLDHHNIIGWTRBGNTA
                                                                                                                                                          NYDMRNIFNGTVVQRHPSHAVTFVDNHDSQPEEALESFVEEWFKPLAYALT
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                                                                                                                          VFYGDMYG--TKGDSQRBIPALKHKIEPILKARKQYAYGAQHDYFDHHDIVGWKREGDSS
                                                                                                                                                                                                                        TROWINHVRSATGKNMFAVAEFWKNDLGAIENYLOKTNWNHSVFDVR
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Title:
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Listing first 45 summaries
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                                                                         SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numata:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhge:*
9: sp_phage:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6 1206.	-				1 1474	0 1614	9 1749	8 1762	7 1766.5	6 1767	5 1836	4 19	3 1946	2 19	1 2061	. Score
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488	484	484	493	481	507	501	613	521	549	549	516	513	533	513	519	Query Match Length DB
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Q8E696	QBDPC8	Q97Q49	Q03657	TAX68D	Q87HG6	Q93I48	Q59222	P71034	Q9KWY6	031193	082839	Q81YJ4	Q9AQ54	Q81AS4	Q9RQT8	ij
Q8e696 streptococc	Q8dpc8 streptococc	Q97q49 streptococc	Q03657 bacillus ci	Q89ypl bacteroides	Q87hg6 vibrio para	Q93148 bacillus sp	Q59222 bacillus sp	P71034 bacillus sp	Q9kwy6 bacillus st	O31193 bacillus st	O82839 bacillus sp	Q81yj4 bacillus an	Q9aq54 bacillus me	Q81as4 bacillus ce	Q9rqt8 cytophaga s	Description

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416	421	420	906	887	826	432	473	461	460	460	457	461	461	469	495	495	495	495	494	506	529	491	485	486	484	492	486	488	
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## ALIGNMENTS

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2 NGTLMQYFEWYTPNDGQHWKKLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61    :	Query Match  78.5%; Score 2061; DB 2; Length 519; Best Local Similarity 75.4%; Pred. No. 3.8e-134; Matches 361; Conservative 48; Mismatches 70; Indels 0; Gaps	SIGNAL 1 57 POTENTIAL. CHAIN 58 519 RAW STARCH DIGESTING AMYLASE. SEQUENCE 519 AA; 58337 MW; 3E6B8BA4DF98B163 CRC64;	PIAM; PYUULZB; ALDHAAMYLASE. PRINTS; PRO0110; ALPHAAMYLASE. SMART; SM00642; Aamy; 1.	06589; Alp_amyl_c 06046; Glyco_hydr	നറ		(1) SEQUENCE FROM N.A. Teams C I. Chen M Y :	idetes; Sph Cytophaga.	QyKUTB; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UN-2003 (TrEMBLrel. 24, Last annotation update) Raw starch disesting amylase precursor.	RESULT 1 Q9RQT8 PRELIMINARY; PRT; 519 AA.
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081AS4;
01-XUN-2003
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Overbeek R., Kyrpides N.
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Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus
Chu L., Mazur M., Goltbynan E., Larseen N., D'Souza M., Walnnas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                      Glycosidase; Hydrolase; Complete proteome 
SEQUENCE 513 AA; 58306 MW; 05C4611C4BFFRFF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cèreus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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LGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHXAGADANEDVTAVEVNPA
                                                                             NGTLMQYFEWYTENDGQHWKRLQNDAEHLSDIGITAVWIPPANKGLSQSDNGYGPYDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    003 (TrEMBLrel. 24, Created)
103 (TrEMBLrel. 24, Last sequence update)
103 (TrEMBLrel. 25, Last annotation update)
4-alpha-maltohexaosidase (EC 3.2.1.98).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDWVDNARAATGKEMFTVGEYWONDLGALNNYLAKVNYNOSLFDAPLHYNFYAASTGGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGEFNQKGTVRTKYGTKGELKSAVNTLHSNGIQVYGDVVMHKAGADYTENVTAVEVNPS
                                                                                                                                                                                           74.2%;
llarity 71.8%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus
                                                                                                                                                                                           Score 1947; DB
Pred. No. 2.8e-J
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comparative
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                                                                                                                                                                                           Gaps
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Best Local
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Q9AQ54
Q9AQ54;
01-JUN-2001
01-JUN-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                  GO; GO:0004556; F:alpha-amylase activity (GO; GO:000575; F:catbohydrate metaboll (InterPro; IPR006047; Alpha amyl car. InterPro; IPR006589; Alp amyl cat_sub. Pfam; PF00128; alpha-amylase; I. SMART; SM0642; Aamy; 1. SMART; SM0642; Aamy; 1. SMART; SM06452; Aamy; 1. SMART; SM06452; Aamy; 1. T89CECD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF220440; AAI
HSSP; P06278; 1VJS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium.
Bacteria; Firmicutes; Bacilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2000) to the EMBL/GerBank/DDBJ EMBL; AF220440; AAK00598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Kim Y.B., Lee B.N., Park K.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of maltopentaose-producing
                                                                                                                                                                                                                                                 Similarity
                                                                                                 LGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAQADATEDVTAVEVNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRNQETSEEYQIKAWTDERFPGRGNTYSDEKWHWYHFDGADWDESRKISRIFKFRGEGKA 181
                              NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISKIFKFRGEGKA
                                                                                                                                                                    NGTLMQYFEWYTPNDGOHWKRLONDAEHLSDIGITAVWIPAAYKGLSQSDNGYGFYDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGLAALITDÓÞGGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYGDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDMARLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRIVEVSGDYEISAWIGFNFPGRGDSYSNFKWKWYHFDGIDWDEGRKLNRIYKFRGIGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGEFNQKGTVRTKYGTKAQLKSAIDALHKKNIDVYGDVVMNHKGGADYTETVTAVEVDPS
NRNVEVSGDYEISAWIGENFPGRGDSYSNFKWKWYHFDGIDWDEGRKLNRI
                                                                         LGEFNQKGTVRTKYGTKAQLKSAIDALHKKNIDVYGDVVMNHKGGAD
                                                                                                                                                    NGTLMOYFEWYAPNDGNHWNRLRTDAENLAQKGITSVWIPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDWEVSSENGNYDYLMYADLDFDHPDVANEMKKWGTWYANELNLDGFRLDAVKHIDHEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VNHVRQQTGKEMFTVAEYWQNDIQTLNNYLAKVNYNQSVFDAFLHYNFHYASTGNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lkgtvvanhptlavtlvenhdsqpgqslesvvspwfkplayafiltraegypsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TXGTSPXEIPSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTREGDSSAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Son
                                                                                                                                                                                                                                               74.2%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAKWMDVGKUNAGEVWYDITGNQTNTVTINKDGWGQFQVSGGSVSIY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H.J.,
                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                           Score 1946; DB\
Pred. No. 3.5e-1
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 es;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                        789CECD6A19CVDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                  Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus
                                                                                                                                                                                                                               Indels
                                                                                                                                                    KGTTQNDVGYGAYDLYD
                                                                           TETVIAVEVDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    megaterium
                                                                                                                                                                                                                               <u>.</u>
GRGIGKA
                                                                                                                                                                                                                             Gaps
                                      181
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241

472 VNGGSVSVWV

481

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RESULT 7
                                                                                                                                                                                                                                                                                                   InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR002044; CBD_4.
InterPro; IPR006046; Glyco hydro_13.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007299; IPT TIG.
Pfam; PP00128; Alpha-amylase; 1.
Pfam; PP00186; Glyco hydro_15
Pfam; PP00189; IPT TIG.
Pfam; PP00189; Alpha-amylase; 1.
Pfam; PP00189; IPT TIG.
Pfam; PP00189; Alpha-amylase; 1.
Pfam; PP00189; IPT TIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel.-26, Last sequence update)
10-OCT-2003 (Rek: 42, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
(Cyclodextrin-glycosyltransferase) (CGTase).
CGT.
 DOMAIN
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -II- SUBUNIT: MODOMET.

-I- MISCELLANGOUS: CCTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
-IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
-I- SIMILARITY: Belongs to family 13 of 91ycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucanotransferases and analysis of the thermal stabilities and pH optima of the enzymes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
MEDLINE=90257592; PubMed=2534600;
Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;
"Construction of a chimeric series of Bacillus cyclomaltodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sp. (strain 17-1).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                          DOMAIN
                                                                                         DOMAIN
                                                                                                                                                                     SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy C; 1.
                                                                                                                                                                                                           PRINTS; PR00110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28053; AAA22310.1; -. HSSP; P43379; 1CDG.
                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1409;
                                                                                                                                                              Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. <u>Microbiol.</u> 135:3447-3457(1989).

CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a 1,4-alpha-D-glucosidic bond.

COFACTOR: Binds 2 calcium ions per subunit (By similarity).
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   Glycosy
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                    27
713
165
229
229
609
713
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                                                                                                                                                            transferase; Calcium-binding; Signal.
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
A1.
B.
A2.
C.
D.
B.
BY SIMILARITY.
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AMYB\_PABPO P21543; 01-MAY-1991

STANDARD

PRT; 1196

15-MAR-2004 Beta/alpha

1 (Rel. 28, Created)
1 (Rel. 18, Last sequence update)
4 (Xel. 4) Last annotation update)
-Amylase provursor [Includes: Beta-amylase (EC 3.2.1.1);
ase (EC 3.2.1.1).

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AMYB.
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            RESULT
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Best Local Sim
Matches 135;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                184 LYNNGRDE---GGY-----TNDTHNLF----HHNGGTDFS------
                                                                                 493 -PITTRP
                                                                                                            483
                                                                                                                                     438 MYVGKQHAGKVFYDLTGN--RSDTVTINSDGWGE-FKVNGGSVSVW-VPRKTTVSTIAR- 492
                                                                                                                                                                                            388 LIARRDYAYGTQHDYLDH$DIIGWTREGGTE------KPGSGLAALITDGPGGSKW 437
                                                                                                                                                                                                                         372 --ALAFTLT-SRGVPAI\---YYGTEQYMSGGNDFDNRARIPSFSTTTTAYQVSKKLAPL
                                                                                                                                                                                                                                                 348 PLAYAFILTRQEGYPCVFYGDYYGIPQY------NIPS------LKSKIDPL 387
                                                                                                                                                                                                                                                                             319 VFKDNTDNMYGLKSMLEGSATDYAQMEDO----VTFIDNHDMERFHNNSANRRKLEO---
                                                                                                                                                                                                                                                                                                        298 ASK--SGGAFDMRTLMTNTL-----MKDQPTLAVTFVDNHDTE---PGQALQSWVDPWFK 347
                                                                                                                                                                                                                                                                                                                                    262 PFGWQKSFMATVNNY--KFVFTFGE-WFLGVNEVSAENHKFANVSGMSLLDFRFAQKVRQ 318
                                                                                                                                                                                                                                                                                                                                                            240 KESFEPDWLSYVRSQTGKPLFTVGEYWSYDINKL--HNYITKTDGTMSLFDAPLHNKFYT 297
                                                       532 GPMMAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                IGKAWDWEVDTENGNYDYLM-YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDIGEFNOKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGA--DGTEWVDAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YWARDFKK---TNPAYGTIADFQNLIAAAHAKNIKVIIDFAPNHTSPASLDQPSFAENGK 183
                                                                                                                                                                RKSNPAIAYGTTQERWINIDVLIYERKFGNNVAVIAVNRNVNTSASITGLVTSLPAGS--
                                                                                                                                                                                                                                                                                                                                                                                         -----TTENGIYKNLYDLADLNHNNSTVDTYLKDAIKWWLD-LGIDGIRMDAVKHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         713 AA;
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166
217
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78
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                                                                                                              ----ytdvlggllngnnltvgsggsasiftlaaggtavwqyttavtaptighv 531
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77389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 313; DB 1; Length 713;
24.7%; Pred. No. 8.6e-15;
tive 82; Mismatches 188; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM
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BY SIMILARITY.
CALCIUM 2 (BY SIMILARITY).
CALCIUM 2 (VIA CARBONYL OXYGEN)
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CALCIUM 1 (VIA CARBONYL OXYGEN)
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2 (BY SIMILARITY).
2 (VIA CARBONYL OXYGEN)
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